GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 17, 2003, 09:18:53 ; Search time 0.001 Seconds
(without alignments)
17.960 Million cell updates/sec

Title: us-10-008-789-22
Perfect score: 20
Sequence: 1 gcttcagggagcccgtgcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 52 seqs, 449 residues

Total number of hits satisfying chosen parameters: 104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 53 summaries

Database : rni.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	10.4	52.0	13	1	US-08-259-148A-60	Sequence 60, Appl
c	2	10.4	52.0	13	1	US-07-876-941A-76	Sequence 76, Appl
c	3	8	40.0	10	1	US-08-202-927-21	Sequence 21, Appl
c	4	8	40.0	10	1	US-09-424-518-1	Sequence 1, Appli
c	5	8	40.0	10	1	PCT-US95-02419-21	Sequence 21, Appl
	6	7.4	37.0	9	1	US-08-566-037A-21	Sequence 21, Appl
	7	7	35.0	8	1	US-08-859-954-86	Sequence 86, Appl
c	8	7	35.0	8	1	US-08-859-954-346	Sequence 346, App
c	9	7	35.0	8	1	US-08-859-954-347	Sequence 347, App
c	10	7	35.0	9	1	US-08-331-398A-37	Sequence 37, Appl
c	11	7	35.0	9	1	US-08-331-397B-37	Sequence 37, Appl
c	12	7	35.0	9	1	US-08-759-804A-37	Sequence 37, Appl
c	13	7	35.0	9	1	US-09-227-693-37	Sequence 37, Appl
c	14	7	35.0	9	1	US-09-528-760A-18	Sequence 18, Appl
	15	7	35.0	9	1	US-09-528-760A-19	Sequence 19, Appl
c	16	7	35.0	9	1	US-09-397-992A-32	Sequence 32, Appl
	17	7	35.0	9	1	US-09-397-992A-33	Sequence 33, Appl
c	18	7	35.0	9	1	US-09-526-416-3	Sequence 3, Appli
	19	7	35.0	9	1	US-09-526-416-4	Sequence 4, Appli
c	20	7	35.0	9	1	US-09-472-130A-13	Sequence 13, Appl
	21	7	35.0	9	1	US-09-472-130A-14	Sequence 14, Appl
c	22	7	35.0	9	1	US-09-971-843-32	Sequence 32, Appl
	23	7	35.0	9	1	US-09-971-843-33	Sequence 33, Appl
c	24	7	35.0	9	1	US-09-951-843-18	Sequence 18, Appl
	25	7	35.0	9	1	US-09-951-843-19	Sequence 19, Appl
	26	6.4	32.0	8	1	US-08-232-144-10	Sequence 10, Appl
	27	6.4	32.0	8	1	US-08-480-473B-32	Sequence 32, Appl
c	28	6.4	32.0	8	1	US-08-480-473B-34	Sequence 34, Appl
	29	6.4	32.0	8	1	US-08-915-213-32	Sequence 32, Appl
c	30	6.4	32.0	8	1	US-08-915-213-34	Sequence 34, Appl
	31	6.4	32.0	8	1	US-08-646-301A-10	Sequence 10, Appl
	32	6.4	32.0	8	1	US-09-235-217-32	Sequence 32, Appl
c	33	6.4	32.0	8	1	US-09-235-217-34	Sequence 34, Appl
c	34	6.4	32.0	8	1	US-09-544-713-4	Sequence 4, Appli
	35	6.4	32.0	8	1	PCT-US96-10251-32	Sequence 32, Appl
c	36	6.4	32.0	8	1	PCT-US96-10251-34	Sequence 34, Appl
	37	6.4	32.0	8	1	5179003-1	Patent No. 5179003
c	38	6.4	32.0	8	1	5179003-1	Patent No. 5179003
	39	6	30.0	8	1	US-08-574-586-6	Sequence 6, Appli
c	40	6	30.0	8	1	US-08-593-345B-15	Sequence 15, Appl
	41	6	30.0	8	1	US-08-480-473B-31	Sequence 31, Appl
	42	6	30.0	8	1	US-09-069-434-6	Sequence 6, Appli
	43	6	30.0	8	1	US-09-069-434-11	Sequence 11, Appl
	44	6	30.0	8	1	US-09-069-434-12	Sequence 12, Appl
	45	6	30.0	8	1	US-08-915-213-31	Sequence 31, Appl
	46	6	30.0	8	1	US-08-859-954-85	Sequence 85, Appl
	47	6	30.0	8	1	US-08-859-954-87	Sequence 87, Appl
c	48	6	30.0	8	1	US-08-859-954-95	Sequence 95, Appl
	49	6	30.0	8	1	US-08-859-954-338	Sequence 338, App
c	50	6	30.0	8	1	US-08-859-954-348	Sequence 348, App
c	51	6	30.0	8	1	US-08-859-954-510	Sequence 510, App
	52	6	30.0	8	1	US-09-235-217-31	Sequence 31, Appl
	53	6	30.0	8	1	PCT-US96-10251-31	Sequence 31, Appl

ALIGNMENTS

```
RESULT 1
US-08-259-148A-60/c
; Sequence 60, Application US/08259148A
; Patent No. 5741490
;  GENERAL INFORMATION:
;    APPLICANT:  Reyes, Gregory R.
;    APPLICANT:  Bradley, Daniel W.
;    APPLICANT:  Twu, Jr-Shin
;    APPLICANT:  Purdy, Michael A.
;    APPLICANT:  Tam, Albert W.
;    APPLICANT:  Krawczynski, Krzysztof Z.
;    APPLICANT:  Yarbough, Patrice D.
;    TITLE OF INVENTION:  Hepatitis E Virus Vaccine and Method
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/259,148A
;      FILING DATE:  13-JUN-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 822,335
;      FILING DATE:  17-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 505,888
;      FILING DATE:  05-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 420,921
;      FILING DATE:  13-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 367,486
;      FILING DATE:  16-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 336,672
;      FILING DATE:  11-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 208,997
;      FILING DATE:  17-JUN-1988
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  4600-0093.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  DNA sequence, Fig. 7
US-08-259-148A-60

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 0.59;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCCCG 15
              ||||||||| ||
Db         13 TCAGGGAGCGCG 2


RESULT 2
US-07-876-941A-76/c
; Sequence 76, Application US/07876941A
; Patent No. 5885768
;  GENERAL INFORMATION:
;    APPLICANT:  Reyes, Gregory R.
;    APPLICANT:  Bradley, Daniel W.
;    APPLICANT:  Tam, Albert W.
;    APPLICANT:  Mitchell, Carl
;    TITLE OF INVENTION:  Hepatitis E Virus Peptide Antigen and
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/876,941A
;      FILING DATE:  01-MAY-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 822,335
;      FILING DATE:  17-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 505,888
;      FILING DATE:  05-APRIL-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 420,921
;      FILING DATE:  13-OCTOBER-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 367,486
;      FILING DATE:  16-JUNE-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 336,672
;      FILING DATE:  11-APRIL-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 208,997
;      FILING DATE:  17-JUNE-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  4600-0093.33
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  76:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  DNA sequence, Fig. 7
US-07-876-941A-76

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 0.59;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCCCG 15
              ||||||||| ||
Db         13 TCAGGGAGCGCG 2


RESULT 3
US-08-202-927-21/c
; Sequence 21, Application US/08202927
; Patent No. 5646126
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Yung-chi
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Meyer Jr., Rich B.
;    APPLICANT:  Pai, Balakrishna S.
;    APPLICANT:  Reed, Michael W.
;    APPLICANT:  Zhou, James H.
;    TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
;    TITLE OF INVENTION:  Anticancer Activity
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klein & Szekeres
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,927
;      FILING DATE:  28-FEB-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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      TOPOLOGY:
    FEATURE:      linear
      NAME/KEY:
      LOCATIO:  modified_base
      OTHER N:  10
      OTHER INFORMATION:  /mod_base= OTHER
      OTHER INFORMATION:  /note= "Nucleotide 10 has a tail which comprises
      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
US-08-2 OTHER INFORMATION:  formula 3)."
      02-927-21

  Quer
  Best Match              40.0%;  Score 8;  DB 1;  Length 10;
  Mat( Local Similarity   100.0%;  Pred. No. 2.4;
    hes    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CCCGTGCG 19
               ||||||||
Db           8 CCCGTGCG 1


R
ULT 4
-09-424-518-1/c
Sequence 1, Application US/09424518
Patent No. 6260034
GENERAL INFORMATION:
 APPLICANT:  Bjorkesten, Lennart
 TITLE OF INVENTION:  A Method and a System for Nucleic Acid Sequence Analysis
Patent No. 6260034
 FILE REFERENCE:  45687-00004
 CURRENT APPLICATION NUMBER: US/09/424,518
 CURRENT FILING DATE:  1999-11-23
 PRIOR APPLICATION NUMBER:  PCT/SE98/01005
 PRIOR FILING DATE:  1998-05-27
 PRIOR APPLICATION NUMBER:  9702008-5
 PRIOR FILING DATE:  1997-05-28
 NUMBER OF SEQ ID NOS:  1
 SOFTWARE:  PatentIn version 3.0
SEQ ID NO 1
  LENGTH: 10
  TYPE: DNA
  ORGANISM: Homo sapiens
S-09-424-518-1

 Query Match              40.0%;  Score 8;  DB 1;  Length 10;
 Best Local Similarity    100.0%;  Pred. No. 2.4;
 Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

y          1 GCTTCAGG 8
             ||||||||
b          8 GCTTCAGG 1


SULT 5
T-US95-02419-21/c
Sequence 21, Application PC/TUS9502419
 GENERAL INFORMATION:
   APPLICANT:  Cheng, Yung-chi
   APPLICANT:  Lukhtanov, Eugeny A.
   APPLICANT:  Meyer Jr., Rich B.
   APPLICANT:  Pai, Balakrishna S.
   APPLICANT:  Reed, Michael W.
   APPLICANT:  Zhou, James H.
   TITLE OF INVENTION:  Modified Oligonucleotide Duplexes Having
   TITLE OF INVENTION:  Anticancer Activity
   NUMBER OF SEQUENCES:  70
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Klein & Szekeres
     STREET:  4199 Campus Drive, Suite 700
     CITY:  Irvine
     STATE:  CA
     COUNTRY:  U.S.A.
```

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;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02419
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/202,927
;      FILING DATE:  28-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-07-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 854-5502
;      TELEFAX:  (714) 854-4897
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  10
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "Nucleotide 10 has a tail which comprises
;      OTHER INFORMATION:  a cholesterol moiety which has its A ring linked to
;      OTHER INFORMATION:  the 3'-phosphate through a carbonyl group attached
;      OTHER INFORMATION:  to the ring nitrogen of a moiety derived from
;      OTHER INFORMATION:  4-hydroxy-2-hydroxymethylpyrrolidine (see
;      OTHER INFORMATION:  formula 3)."
PCT-US95-02419-21

  Query Match              40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity    100.0%;  Pred. No. 2.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CCCGTGCG 19
               ||||||||
Db           8 CCCGTGCG 1


RESULT 6
US-08-566-037A-21
; Sequence 21, Application US/08566037A
; Patent No. 5756295
;  GENERAL INFORMATION:
;    APPLICANT:  Haruo ONDA et al.
;    TITLE OF INVENTION:  DNA PRIMER AND A METHOD FOR
;    TITLE OF INVENTION:  SCREENING DNAS
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/566,037A
;      FILING DATE:  December 1, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
```

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Synthetic DNA
!S-08-566-037A-21

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          5 CAGGGAGCC 13
              || ||||||
Db          1 CATGGAGCC 9
```

RESULT 7
US-08-859-954-86
; Sequence 86, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; URRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; LASSIFICATION:
; OR APPLICATION DATA:
; PRIOLICATION NUMBER: 08/632,782
; APING DATE:
; FILEY/AGENT INFORMATION:
; ATTORN Paul, Thomas D.
; NAME:RATION NUMBER: 32,714
; REGIS:NCE/DOCKET NUMBER: D-5900
; REFERENICATION INFORMATION:
; TELECOMM:E: 713/651-5325
; TELEPHON 713/651-5246
; TELEFAX: OR SEQ ID NO: 86:
; INFORMATION RACTERISTICS:
; SEQUENCE CHA base pairs
; LENGTH: 8 eic acid
; TYPE: nucl: single
; STRANDEDNESS near
; TOPOLOGY: li other nucleic acid
; MOLECULE TYPE:
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-86

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCTTCAG 7
              |||||||
Db          1 GCTTCAG 7
```

RESULT 8
US-08-859-954-346/c
; Sequence 346, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 346:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-346

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTTCAGG 8
              |||||||
Db          7 CTTCAGG 1
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RESULT 9

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US-08-859-954-347/c
; Sequence 347, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  347:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-347

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGG 8
              |||||||
Db          7 CTTCAGG 1


RESULT 10
US-08-331-398A-37/c
; Sequence 37, Application US/08331398A
; Patent No. 5608039
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Willingham, Mark
;    APPLICANT:  FitzGerald, David
;    APPLICANT:  Brinkmann, Ulrich
;    APPLICANT:  Pai, Lee
;    TITLE OF INVENTION:  Single Chain B3 Antibody Fusion Proteins
;    TITLE OF INVENTION:  and Their Uses (as amended)
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/331,398A
;      FILING DATE:  28-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  015280-126110US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-331-398A-37

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          9 CAGGGAG 3


RESULT 11
US-08-331-397B-37/c
; Sequence 37, Application US/08331397B
; Patent No. 5981726
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Benhar, Itai
;    TITLE OF INVENTION:  Chimeric and Mutationally Stabilized Tumor-
;    TITLE OF INVENTION:  Specific Antibody Fragments, Fusion Proteins, and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/331,397B
;      FILING DATE:  28-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
```

```
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  015280-126120US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-331-397B-37

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          9 CAGGGAG 3


RESULT 12
US-08-759-804A-37/c
; Sequence 37, Application US/08759804A
; Patent No. 5990296
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Willingham, Mark
;    APPLICANT:  FitzGerald, David J.
;    APPLICANT:  Brinkmann, Ulrich
;    APPLICANT:  Pai, Lee
;    TITLE OF INVENTION:  Tumor-Specific Antibody Fragments,
;    TITLE OF INVENTION:  Fusion Proteins, and Uses Thereof
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/759,804A
;      FILING DATE:  03-DEC-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/331,398
;      FILING DATE:  28-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen L.
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  015280-126140US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-759-804A-37

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          9 CAGGGAG 3


RESULT 13
US-09-227-693-37/c
; Sequence 37, Application US/09227693
; Patent No. 6287562
;  GENERAL INFORMATION:
;    APPLICANT:  PASTAN, Ira
;    APPLICANT:  BENHAR, Itai
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  JUNG, Sun-Hee
;    APPLICANT:  LEE, Byungkook
;    TITLE OF INVENTION:  HUMANIZED TUMOR-SPECIFIC ANTIBODY
;    TITLE OF INVENTION:  FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/227,693
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/331,396
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  15280-126-1-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-227-693-37

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
```

```
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 18
US-09-526-416-3/c
; Sequence 3, Application US/09526416
; Patent No. 6399351
; GENERAL INFORMATION:
;  APPLICANT:  Bjornvad, Mads E.
;  APPLICANT:  Andersen, Jens T.
;  APPLICANT:  Schnorr, Kirk
;  APPLICANT:  Schulein, Martin
;  APPLICANT:  Kongsbak, Lars
;  TITLE OF INVENTION:  No. 6399351el Pectate Lyases
;  FILE REFERENCE:  5839.200-US
;  CURRENT APPLICATION NUMBER: US/09/526,416
;  CURRENT FILING DATE:  2000-03-15
;  PRIOR APPLICATION NUMBER:  PA 1999 00367
;  PRIOR FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER:  60/124,969
;  PRIOR FILING DATE:  1999-03-18
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-526-416-3

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 19
US-09-526-416-4
; Sequence 4, Application US/09526416
; Patent No. 6399351
; GENERAL INFORMATION:
;  APPLICANT:  Bjornvad, Mads E.
;  APPLICANT:  Andersen, Jens T.
;  APPLICANT:  Schnorr, Kirk
;  APPLICANT:  Schulein, Martin
;  APPLICANT:  Kongsbak, Lars
;  TITLE OF INVENTION:  No. 6399351el Pectate Lyases
;  FILE REFERENCE:  5839.200-US
;  CURRENT APPLICATION NUMBER: US/09/526,416
;  CURRENT FILING DATE:  2000-03-15
;  PRIOR APPLICATION NUMBER:  PA 1999 00367
;  PRIOR FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER:  60/124,969
;  PRIOR FILING DATE:  1999-03-18
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-526-416-4

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 20
US-09-472-130A-13/c
; Sequence 13, Application US/09472130A
; Patent No. 6473765
; GENERAL INFORMATION:
;  APPLICANT: Xu, Wenfeng
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Yee, David P.
;  APPLICANT:  Foster, Donald C.
;  TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
;  TITLE OF INVENTION:  (ZCHEMR2)
;  FILE REFERENCE: 98-10D2
;  CURRENT APPLICATION NUMBER: US/09/472,130A
;  CURRENT FILING DATE:  2000-01-07
;  PRIOR APPLICATION NUMBER: US 09/053,866
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-472-130A-13

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 21
US-09-472-130A-14
; Sequence 14, Application US/09472130A
; Patent No. 6473765
; GENERAL INFORMATION:
;  APPLICANT: Xu, Wenfeng
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Yee, David P.
;  APPLICANT:  Foster, Donald C.
;  TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
;  TITLE OF INVENTION:  (ZCHEMR2)
;  FILE REFERENCE: 98-10D2
;  CURRENT APPLICATION NUMBER: US/09/472,130A
;  CURRENT FILING DATE:  2000-01-07
;  PRIOR APPLICATION NUMBER: US 09/053,866
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-472-130A-14

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          9 CAGGGAG 3


RESULT 14
US-09-528-760A-18/c
; Sequence 18, Application US/09528760A
; Patent No. 6312924
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11
;  CURRENT APPLICATION NUMBER: US/09/528,760A
;  CURRENT FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-528-760A-18

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 15
US-09-528-760A-19
; Sequence 19, Application US/09528760A
; Patent No. 6312924
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11
;  CURRENT APPLICATION NUMBER: US/09/528,760A
;  CURRENT FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-528-760A-19

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 16
US-09-397-992A-32/c
; Sequence 32, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46
;  CURRENT APPLICATION NUMBER: US/09/397,992A
;  CURRENT FILING DATE:  1999-09-16
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-397-992A-32

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 17
US-09-397-992A-33
; Sequence 33, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46
;  CURRENT APPLICATION NUMBER: US/09/397,992A
;  CURRENT FILING DATE:  1999-09-16
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-397-992A-33

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-951-843-19

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 26
US-08-232-144-10
; Sequence 10, Application US/08232144
; Patent No. 5571695
;  GENERAL INFORMATION:
;    APPLICANT:  SELBIE, Lisa
;    APPLICANT:  HERZOG, Herbert
;    APPLICANT:  SHINE, John
;    TITLE OF INVENTION:  Human Neuropeptide Y-Y1 Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rothwell, Figg, Ernst & Kurz
;      STREET:  555 13th St, N.W., Suite 701-East
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,144
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, Barbara G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1871-107A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-783-6040
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
US-08-232-144-10

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCC 14
              | ||||||
Db          1 GCGAGCCC 8


RESULT 27
US-08-480-473B-32
; Sequence 32, Application US/08480473B
; Patent No. 5882914
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,473B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-480-473B-32

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CCCGTGCG 19
              | ||||||
Db          1 CACGTGCG 8


RESULT 28
US-08-480-473B-34/c
; Sequence 34, Application US/08480473B
; Patent No. 5882914
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,473B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  34:
```

```
Qy          12 CCCGTGC 18
               |||||||
Db           1 CCCGTGC 7


RESULT 22
US-09-971-843-32/c
; Sequence 32, Application US/09971843
; Patent No. 6544505
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46D1
;  CURRENT APPLICATION NUMBER: US/09/971,843
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 09/397,992
;  PRIOR FILING DATE: 1999-09-16
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-971-843-32

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CCCGTGC 18
               |||||||
Db           9 CCCGTGC 3


RESULT 23
US-09-971-843-33
; Sequence 33, Application US/09971843
; Patent No. 6544505
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46D1
;  CURRENT APPLICATION NUMBER: US/09/971,843
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 09/397,992
;  PRIOR FILING DATE: 1999-09-16
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-971-843-33

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CCCGTGC 18
               |||||||
Db           1 CCCGTGC 7


RESULT 24
US-09-951-843-18/c
; Sequence 18, Application US/09951843
; Patent No. 6548056
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11D1
;  CURRENT APPLICATION NUMBER: US/09/951,843
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: 09/528,760
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-951-843-18

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CCCGTGC 18
               |||||||
Db           9 CCCGTGC 3


RESULT 25
US-09-951-843-19
; Sequence 19, Application US/09951843
; Patent No. 6548056
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11D1
;  CURRENT APPLICATION NUMBER: US/09/951,843
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: 09/528,760
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 9
;   TYPE: DNA
```

```
  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 14;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCC 14
              |:::|:||
Db          1 GSSWGSCC 8


RESULT 32
US-09-235-217-32
; Sequence 32, Application US/09235217
; Patent No. 6222018
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/235,217
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-235-217-32

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CCCGTGCG 19
              | ||||||
Db          1 CACGTGCG 8


RESULT 33
US-09-235-217-34/c
; Sequence 34, Application US/09235217
; Patent No. 6222018
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/235,217
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-235-217-34

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGCCCGTG 17
              ||| ||||
Db          8 AGCACGTG 1


RESULT 34
US-09-544-713-4/c
; Sequence 4, Application US/09544713
; Patent No. 6261782
; GENERAL INFORMATION:
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Guerra, Cesar E.
;  APPLICANT:  Weber, Shane C.
;  APPLICANT:  Kaufman, Joseph C
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION:  Fixed Address Analysis of Sequence Tags
; Patent No. 6261782
;  FILE REFERENCE:  YU 126
;  CURRENT APPLICATION NUMBER: US/09/544,713
;  CURRENT FILING DATE:  2000-04-06
;  PRIOR APPLICATION NUMBER:  60/127,932
;  PRIOR FILING DATE:  1999-04-06
;  NUMBER OF SEQ ID NOS:  79
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
;   OTHER INFORMATION: Fragment
US-09-544-713-4

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-480-473B-34

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGCCCGTG 17
              ||| ||||
Db          8 AGCACGTG 1


RESULT 29
US-08-915-213-32
; Sequence 32, Application US/08915213
; Patent No. 6020462
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/915,213
;      FILING DATE:  20-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-915-213-32

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CCCGTGCG 19
              | ||||||
Db          1 CACGTGCG 8


RESULT 30
US-08-915-213-34/c
; Sequence 34, Application US/08915213
; Patent No. 6020462
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/915,213
;      FILING DATE:  20-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-915-213-34

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGCCCGTG 17
              ||| ||||
Db          8 AGCACGTG 1


RESULT 31
US-08-646-301A-10
; Sequence 10, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
;  APPLICANT:  Richards, Cynthia Ann
;  APPLICANT:  Huber, Brian E.
;  TITLE OF INVENTION:  Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
;  TITLE OF INVENTION:  Antigen for Expression Targeting
;  FILE REFERENCE:  PB1508USW
;  CURRENT APPLICATION NUMBER: US/08/646,301A
;  CURRENT FILING DATE:  1996-05-16
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  consensus
;   OTHER INFORMATION: sequence B4  from DNA Sequence 1:3-11 (1990).
; Patent No. 6194211
US-08-646-301A-10
```

```
RESULT 39
US-08-574-586-6
; Sequence 6, Application US/08574586
; Patent No. 5837512
;  GENERAL INFORMATION:
;    APPLICANT:  Rabson, ArnoldRichard B.
;    APPLICANT:  Lin, Hsin-Ching
;    APPLICANT:  Bodkin, Marion
;    APPLICANT:  Strair, Roger
;    TITLE OF INVENTION:  Selective Biological Destruction of
;    TITLE OF INVENTION:  Tumor Cells
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices
;      STREET:  758 Springfield avenue
;      CITY:  Summit
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07901
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/574,586
;      FILING DATE:  14-DEC-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Muccino, Richard R.
;      REGISTRATION NUMBER:  32,538
;      REFERENCE/DOCKET NUMBER:  UMD1-026cip
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-273-4988
;      TELEFAX:  908-273-4679
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-574-586-6

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GAGCCC 14
              ||||||
Db          1 GAGCCC 6


RESULT 40
US-08-593-345B-15/c
; Sequence 15, Application US/08593345B
; Patent No. 5851772
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Lysov, Yuriy P
;    APPLICANT:  Shick, Valentine V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  A Microchip Method for the Enrichment of
;    TITLE OF INVENTION:  Specific DNA Sequences.
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/593,345B
;      FILING DATE:  29-JAN-96
;    PRIOR APPLICATION DATA:  No. 5851772e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-029+30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 5851772 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    FEATURE:
;      NAME/KEY:  No. 5851772e
;      LOCATION:  1-8
;      IDENTIFICATION METHOD:  Similarity with known sequences.
;      OTHER INFORMATION:  Complementarity with primer of
;      OTHER INFORMATION:  exons to a-thalassemia gene.
US-08-593-345B-15

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGA 10
              ||||||
Db          6 CAGGGA 1


RESULT 41
US-08-480-473B-31
; Sequence 31, Application US/08480473B
; Patent No. 5882914
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,473B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
```

```
Qy          12 CCCGTGCG 19
               ||| ||||
Db           8 CCCATGCG 1


RESULT 35
PCT-US96-10251-32
; Sequence 32, Application PC/TUS9610251
;  GENERAL INFORMATION:
;    APPLICANT:  The Johns Hopkins University School of Medicine
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10251
;      FILING DATE:  06-JUN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US96-10251-32

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 CCCGTGCG 19
               | ||||||
Db           1 CACGTGCG 8


RESULT 36
PCT-US96-10251-34/c
; Sequence 34, Application PC/TUS9610251
;  GENERAL INFORMATION:
;    APPLICANT:  The Johns Hopkins University School of Medicine
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10251
;      FILING DATE:  06-JUN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US96-10251-34

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          10 AGCCCGTG 17
               ||| ||||
Db           8 AGCACGTG 1


RESULT 37
5179003-1
;Patent No. 5179003
;    APPLICANT: WOLF, DIETER H.;KOPETZKI, ERHARD;SCHUMACHER, GUNTHER
;    TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF PROTEINS OR
;PROTEIN-CONTAINING GENE PRODUCTS
;    NUMBER OF SEQUENCES: 2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/293,502
;      FILING DATE: 04-JAN-1989
;SEQ ID NO:1:
;      LENGTH: 8
5179003-1

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 GGGAGCCC 14
               |||| |||
Db           1 GGGATCCC 8


RESULT 38
5179003-1/c
;Patent No. 5179003
;    APPLICANT: WOLF, DIETER H.;KOPETZKI, ERHARD;SCHUMACHER, GUNTHER
;    TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF PROTEINS OR
;PROTEIN-CONTAINING GENE PRODUCTS
;    NUMBER OF SEQUENCES: 2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/293,502
;      FILING DATE: 04-JAN-1989
;SEQ ID NO:1:
;      LENGTH: 8
5179003-1

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 GGGAGCCC 14
               |||| |||
Db           8 GGGATCCC 1
```

```
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,434
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVIDSON, Ross E.
;      REGISTRATION NUMBER:  P-41,698
;      REFERENCE/DOCKET NUMBER:  P-01480US0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5144
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-069-434-12

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGGGAG 11
              ||||||
Db          1 AGGGAG 6


RESULT 45
US-08-915-213-31
; Sequence 31, Application US/08915213
; Patent No. 6020462
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/915,213
;      FILING DATE:  20-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-915-213-31

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 CGTGCG 19
               ||||||
Db           3 CGTGCG 8


RESULT 46
US-08-859-954-85
; Sequence 85, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  85:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-85

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCA 6
              ||||||
Db          1 GCTTCA 6
```

```
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-480-473B-31

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 CGTGCG 19
              ||||||
Db          3 CGTGCG 8


RESULT 42
US-09-069-434-6
; Sequence 6, Application US/09069434
; Patent No. 6017709
;  GENERAL INFORMATION:
;    APPLICANT:  HARDIN, Susan H.
;    APPLICANT:  YING, Jun
;    APPLICANT:  JONES, Leslie Burgan
;    TITLE OF INVENTION:  DNA Replication Templates Stabilized by
;    TITLE OF INVENTION:  Guanine Quartets
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,434
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVIDSON, Ross E.
;      REGISTRATION NUMBER:  P-41,698
;      REFERENCE/DOCKET NUMBER:  P-01480US0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5144
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-069-434-6

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGGGAG 11
              ||||||
Db          3 AGGGAG 8


RESULT 43
US-09-069-434-11
; Sequence 11, Application US/09069434
; Patent No. 6017709
;  GENERAL INFORMATION:
;    APPLICANT:  HARDIN, Susan H.
;    APPLICANT:  YING, Jun
;    APPLICANT:  JONES, Leslie Burgan
;    TITLE OF INVENTION:  DNA Replication Templates Stabilized by
;    TITLE OF INVENTION:  Guanine Quartets
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,434
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVIDSON, Ross E.
;      REGISTRATION NUMBER:  P-41,698
;      REFERENCE/DOCKET NUMBER:  P-01480US0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5144
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-069-434-11

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGGGAG 11
              ||||||
Db          2 AGGGAG 7


RESULT 44
US-09-069-434-12
; Sequence 12, Application US/09069434
; Patent No. 6017709
;  GENERAL INFORMATION:
;    APPLICANT:  HARDIN, Susan H.
;    APPLICANT:  YING, Jun
;    APPLICANT:  JONES, Leslie Burgan
;    TITLE OF INVENTION:  DNA Replication Templates Stabilized by
;    TITLE OF INVENTION:  Guanine Quartets
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
```

```
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  338:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-338

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAG 7
              ||||||
Db          2 CTTCAG 7


RESULT 50
US-08-859-954-348/c
; Sequence 348, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  348:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-348

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGG 8
              ||||||
Db          6 TTCAGG 1


RESULT 51
US-08-859-954-510/c
; Sequence 510, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  510:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-510

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGGGAG 11
              ||||||
Db          7 AGGGAG 2
```

```
RESULT 47
US-08-859-954-87
; Sequence 87, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  87:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-87

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCA 6
              ||||||
Db          1 GCTTCA 6


RESULT 48
US-08-859-954-95/c
; Sequence 95, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  95:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-95

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAG 7
              ||||||
Db          7 CTTCAG 2


RESULT 49
US-08-859-954-338
; Sequence 338, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
```

```
RESULT 52
US-09-235-217-31
; Sequence 31, Application US/09235217
; Patent No. 6222018
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/235,217
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-235-217-31

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 CGTGCG 19
              ||||||
Db          3 CGTGCG 8


RESULT 53
PCT-US96-10251-31
; Sequence 31, Application PC/TUS9610251
;  GENERAL INFORMATION:
;    APPLICANT:  The Johns Hopkins University School of Medicine
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10251
;      FILING DATE:  06-JUN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US96-10251-31

  Query Match             30.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 CGTGCG 19
              ||||||
Db          3 CGTGCG 8


Search completed: November 17, 2003, 09:18:53
Job time : 0.001 secs
```

OM nucleic - nucleic search, using sw model

Run on: November 17, 2003, 09:21:14 ; Search time 0.001 Seconds
(without alignments)
23.640 Million cell updates/sec

Title: us-10-008-789-22
Perfect score: 20
Sequence: 1 gcttcagggagcccgtgcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 63 seqs, 591 residues

Total number of hits satisfying chosen parameters: 126

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 63 summaries

Database : rnpb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	1	US-10-008-789-22	Sequence 22, Appl
2		11.4	57.0	15	1	US-10-133-779-170	Sequence 170, App
3		9	45.0	10	1	US-10-330-627-836	Sequence 836, App
4		9	45.0	10	1	US-10-033-145-625	Sequence 625, App
5		8.4	42.0	10	1	US-10-330-627-779	Sequence 779, App
6		8.4	42.0	10	1	US-10-330-627-780	Sequence 780, App
7	c	8.4	42.0	10	1	US-10-033-145-804	Sequence 804, App
8		8	40.0	10	1	US-10-330-627-455	Sequence 455, App
9	c	8	40.0	10	1	US-10-330-627-855	Sequence 855, App
10		7.4	37.0	9	1	US-09-989-789-2132	Sequence 2132, Ap
11		7.4	37.0	9	1	US-09-989-789-2133	Sequence 2133, Ap
12		7.4	37.0	9	1	US-09-989-789-2134	Sequence 2134, Ap
13		7.4	37.0	9	1	US-09-989-789-2135	Sequence 2135, Ap
14		7.4	37.0	9	1	US-09-990-186-2132	Sequence 2132, Ap
15		7.4	37.0	9	1	US-09-990-186-2133	Sequence 2133, Ap
16		7.4	37.0	9	1	US-09-990-186-2134	Sequence 2134, Ap
17		7.4	37.0	9	1	US-09-990-186-2135	Sequence 2135, Ap
18		7.4	37.0	9	1	US-09-989-994-2132	Sequence 2132, Ap
19		7.4	37.0	9	1	US-09-989-994-2133	Sequence 2133, Ap
20		7.4	37.0	9	1	US-09-989-994-2134	Sequence 2134, Ap
21		7.4	37.0	9	1	US-09-989-994-2135	Sequence 2135, Ap
22	c	7	35.0	9	1	US-09-842-746-1	Sequence 1, Appli
23		7	35.0	9	1	US-09-842-746-2	Sequence 2, Appli
24		7	35.0	9	1	US-09-989-789-2121	Sequence 2121, Ap
25		7	35.0	9	1	US-09-989-789-2122	Sequence 2122, Ap
26		7	35.0	9	1	US-09-989-789-2172	Sequence 2172, Ap
27		7	35.0	9	1	US-09-989-789-2173	Sequence 2173, Ap
28		7	35.0	9	1	US-09-989-789-2186	Sequence 2186, Ap
29		7	35.0	9	1	US-09-989-789-2187	Sequence 2187, Ap
30		7	35.0	9	1	US-09-989-789-2206	Sequence 2206, Ap
31		7	35.0	9	1	US-09-989-789-2244	Sequence 2244, Ap
32	c	7	35.0	9	1	US-09-873-134-5	Sequence 5, Appli
33		7	35.0	9	1	US-09-873-134-6	Sequence 6, Appli
34	c	7	35.0	9	1	US-09-951-843-18	Sequence 18, Appl
35		7	35.0	9	1	US-09-951-843-19	Sequence 19, Appl
36	c	7	35.0	9	1	US-09-971-843-32	Sequence 32, Appl
37		7	35.0	9	1	US-09-971-843-33	Sequence 33, Appl
38		7	35.0	9	1	US-09-990-186-2121	Sequence 2121, Ap
39		7	35.0	9	1	US-09-990-186-2122	Sequence 2122, Ap
40		7	35.0	9	1	US-09-990-186-2172	Sequence 2172, Ap
41		7	35.0	9	1	US-09-990-186-2173	Sequence 2173, Ap
42		7	35.0	9	1	US-09-990-186-2186	Sequence 2186, Ap
43		7	35.0	9	1	US-09-990-186-2187	Sequence 2187, Ap
44		7	35.0	9	1	US-09-990-186-2206	Sequence 2206, Ap
45		7	35.0	9	1	US-09-990-186-2244	Sequence 2244, Ap
46		7	35.0	9	1	US-09-989-994-2121	Sequence 2121, Ap
47		7	35.0	9	1	US-09-989-994-2122	Sequence 2122, Ap
48		7	35.0	9	1	US-09-989-994-2172	Sequence 2172, Ap
49		7	35.0	9	1	US-09-989-994-2173	Sequence 2173, Ap
50		7	35.0	9	1	US-09-989-994-2186	Sequence 2186, Ap
51		7	35.0	9	1	US-09-989-994-2187	Sequence 2187, Ap
52		7	35.0	9	1	US-09-989-994-2206	Sequence 2206, Ap
53		7	35.0	9	1	US-09-989-994-2244	Sequence 2244, Ap
54	c	7	35.0	9	1	US-10-358-619-18	Sequence 18, Appl
55		7	35.0	9	1	US-10-358-619-19	Sequence 19, Appl
56	c	7	35.0	9	1	US-09-873-135-5	Sequence 5, Appli
57		7	35.0	9	1	US-09-873-135-6	Sequence 6, Appli
58	c	7	35.0	9	1	US-10-124-090-5	Sequence 5, Appli
59		7	35.0	9	1	US-10-124-090-6	Sequence 6, Appli
60	c	7	35.0	9	1	US-10-277-494-134	Sequence 134, App
61		7	35.0	9	1	US-10-277-494-212	Sequence 212, App
62	c	7	35.0	9	1	US-10-152-363A-57	Sequence 57, Appl
63		7	35.0	9	1	US-10-152-363A-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-008-789-22
; Sequence 22, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-22

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAGGGAGCCCGTGCGG 20
||||||||||||||||||||
Db 1 GCTTCAGGGAGCCCGTGCGG 20

RESULT 2
US-10-133-779-170
; Sequence 170, Application US/10133779
; Publication No. US20030165884A1
; GENERAL INFORMATION:
; APPLICANT: Chow, Robert
; APPLICANT: Tonai, Richard
; APPLICANT: StemCyte, Inc.
; TITLE OF INVENTION: High Throughput Methods of HLA Typing

```
;  FILE REFERENCE: 020035-000210US
;  CURRENT APPLICATION NUMBER: US/10/133,779
;  CURRENT FILING DATE:  2002-04-25
;  PRIOR APPLICATION NUMBER: US/09/747,391
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/172,768
;  PRIOR FILING DATE: 1999-12-20
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 170
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-133-779-170

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 1.5;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GGAGCCCGTGCGG 20
              ||||| |||||||
Db          1 GGAGCGCGTGCGG 13


RESULT 3
US-10-330-627-836
; Sequence 836, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 836
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-836

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCG 15
              |||||||||
Db          1 GGGAGCCCG 9


RESULT 4
US-10-033-145-625
; Sequence 625, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 625
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-625

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCG 15
              |||||||||
Db          1 GGGAGCCCG 9


RESULT 5
US-10-330-627-779
; Sequence 779, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 779
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-779

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 5.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              ||||||||| |
Db          1 GGGAGCCCCT 10


RESULT 6
US-10-330-627-780
; Sequence 780, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 780
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-780

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 5.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              ||||||||| |
Db          1 GGGAGCCCCT 10
```

```
RESULT 7
US-10-033-145-804/c
; Sequence 804, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 804
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-804

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 5.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              ||| ||||||
Db         10 TCAAGGAGCC 1


RESULT 8
US-10-330-627-455
; Sequence 455, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 455
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-455

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 GCCCGTGC 18
               ||||||||
Db           1 GCCCGTGC 8


RESULT 9
US-10-330-627-855/c
; Sequence 855, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 855
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-855

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAG 11
              ||||||||
Db          9 TCAGGGAG 2


RESULT 10
US-09-989-789-2132
; Sequence 2132, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2132
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2132

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 11
US-09-989-789-2133
; Sequence 2133, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2133
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
```

US-09-989-789-2133

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 12
US-09-989-789-2134
; Sequence 2134, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2134
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2134

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 13
US-09-989-789-2135
; Sequence 2135, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2135
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2135

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 14
US-09-990-186-2132
; Sequence 2132, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2132
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2132

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 15
US-09-990-186-2133
; Sequence 2133, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2133
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2133

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 16
US-09-990-186-2134
; Sequence 2134, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20

```
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2134
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2134

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 17
US-09-990-186-2135
; Sequence 2135, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2135
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2135

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 18
US-09-989-994-2132
; Sequence 2132, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2132
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2132

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 19
US-09-989-994-2133
; Sequence 2133, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2133
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2133

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 20
US-09-989-994-2134
; Sequence 2134, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2134
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2134

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 21
US-09-989-994-2135
```

```
; Sequence 2135, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2135
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2135

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 22
US-09-842-746-1/c
; Sequence 1, Application US/09842746
; Patent No. US20020019049A1
; GENERAL INFORMATION:
;  APPLICANT: Lok, Si
;  TITLE OF INVENTION: Methods for Enhancing the Expression of
;  TITLE OF INVENTION:  a Protein of Interest by Recombinant Host Cells
;  FILE REFERENCE: 99-37
;  CURRENT APPLICATION NUMBER: US/09/842,746
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,760
;  PRIOR FILING DATE: 2000-04-26
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-842-746-1

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 23
US-09-842-746-2
; Sequence 2, Application US/09842746
; Patent No. US20020019049A1
; GENERAL INFORMATION:
;  APPLICANT: Lok, Si
;  TITLE OF INVENTION: Methods for Enhancing the Expression of
;  TITLE OF INVENTION:  a Protein of Interest by Recombinant Host Cells
;  FILE REFERENCE: 99-37
;  CURRENT APPLICATION NUMBER: US/09/842,746
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: US 60/199,760
;  PRIOR FILING DATE: 2000-04-26
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-842-746-2

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 24
US-09-989-789-2121
; Sequence 2121, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2121
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2121

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          1 CAGGGAG 7


RESULT 25
US-09-989-789-2122
; Sequence 2122, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2122
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2122
```

```
  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          1 CAGGGAG 7


RESULT 26
US-09-989-789-2172
; Sequence 2172, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2172
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2172

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 27
US-09-989-789-2173
; Sequence 2173, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2173
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2173

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 28
US-09-989-789-2186
; Sequence 2186, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2186
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2186

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 29
US-09-989-789-2187
; Sequence 2187, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2187
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2187

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 30
US-09-989-789-2206
; Sequence 2206, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 2206
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2206

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 31
US-09-989-789-2244
; Sequence 2244, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2244
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2244

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 32
US-09-873-134-5/c
; Sequence 5, Application US/09873134
; Patent No. US20020098568A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Zcys7: A Member of the Cystatin
;  TITLE OF INVENTION:  Superfamily
;  FILE REFERENCE: 00-38
;  CURRENT APPLICATION NUMBER: US/09/873,134
;  CURRENT FILING DATE:  2001-06-01
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-873-134-5

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 33
US-09-873-134-6
; Sequence 6, Application US/09873134
; Patent No. US20020098568A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Zcys7: A Member of the Cystatin
;  TITLE OF INVENTION:  Superfamily
;  FILE REFERENCE: 00-38
;  CURRENT APPLICATION NUMBER: US/09/873,134
;  CURRENT FILING DATE:  2001-06-01
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-873-134-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 34
US-09-951-843-18/c
; Sequence 18, Application US/09951843
; Patent No. US20020168378A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11D1
;  CURRENT APPLICATION NUMBER: US/09/951,843
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: 09/528,760
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-951-843-18

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3
```

```
RESULT 35
US-09-951-843-19
; Sequence 19, Application US/09951843
; Patent No. US20020168378A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11D1
;  CURRENT APPLICATION NUMBER: US/09/951,843
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: 09/528,760
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-951-843-19

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 36
US-09-971-843-32/c
; Sequence 32, Application US/09971843
; Publication No. US20030013162A1
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46D1
;  CURRENT APPLICATION NUMBER: US/09/971,843
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 09/397,992
;  PRIOR FILING DATE: 1999-09-16
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-971-843-32

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 37
US-09-971-843-33
; Sequence 33, Application US/09971843
; Publication No. US20030013162A1
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46D1
;  CURRENT APPLICATION NUMBER: US/09/971,843
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 09/397,992
;  PRIOR FILING DATE: 1999-09-16
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-09-971-843-33

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 38
US-09-990-186-2121
; Sequence 2121, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2121
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2121

  Query Match           35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
```

```
              |||||||
Db          1 CAGGGAG 7


RESULT 39
US-09-990-186-2122
; Sequence 2122, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2122
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2122

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          1 CAGGGAG 7


RESULT 40
US-09-990-186-2172
; Sequence 2172, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2172
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2172

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 41
US-09-990-186-2173
; Sequence 2173, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2173
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2173

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 42
US-09-990-186-2186
; Sequence 2186, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2186
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2186

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 43
US-09-990-186-2187
; Sequence 2187, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2187
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2187

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 44
US-09-990-186-2206
; Sequence 2206, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2206
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2206

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 45
US-09-990-186-2244
; Sequence 2244, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2244
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2244

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 46
US-09-989-994-2121
; Sequence 2121, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2121
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2121

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          1 CAGGGAG 7


RESULT 47
US-09-989-994-2122
; Sequence 2122, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2122
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2122

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          1 CAGGGAG 7


RESULT 48
US-09-989-994-2172
; Sequence 2172, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
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;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2172
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2172

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 49
US-09-989-994-2173
; Sequence 2173, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2173
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2173

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 50
US-09-989-994-2186
; Sequence 2186, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2186
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2186

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 51
US-09-989-994-2187
; Sequence 2187, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2187
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2187

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 52
US-09-989-994-2206
; Sequence 2206, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2206
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2206

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9
```

```
RESULT 53
US-09-989-994-2244
; Sequence 2244, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2244
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-2244

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 54
US-10-358-619-18/c
; Sequence 18, Application US/10358619
; Publication No. US20030147851A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11D1
;  CURRENT APPLICATION NUMBER: US/10/358,619
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/951,843
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: 09/528,760
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-10-358-619-18

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 55
US-10-358-619-19
; Sequence 19, Application US/10358619
; Publication No. US20030147851A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Feldhaus, Andrew L.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Murine Interferon-Alpha
;  FILE REFERENCE: 99-11D1
;  CURRENT APPLICATION NUMBER: US/10/358,619
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/951,843
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: 09/528,760
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,045
;  PRIOR FILING DATE: 1999-03-18
;  PRIOR APPLICATION NUMBER: 60/155,739
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence.
US-10-358-619-19

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 56
US-09-873-135-5/c
; Sequence 5, Application US/09873135
; Publication No. US20030165838A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Zcys6: A Member of the Cystatin
;  TITLE OF INVENTION:  Superfamily
;  FILE REFERENCE: 00-37
;  CURRENT APPLICATION NUMBER: US/09/873,135
;  CURRENT FILING DATE:  2001-06-01
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-873-135-5

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 57
US-09-873-135-6
; Sequence 6, Application US/09873135
; Publication No. US20030165838A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
```

```
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Zcys6: A Member of the Cystatin
;  TITLE OF INVENTION:  Superfamily
;  FILE REFERENCE: 00-37
;  CURRENT APPLICATION NUMBER: US/09/873,135
;  CURRENT FILING DATE:  2001-06-01
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-09-873-135-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 58
US-10-124-090-5/c
; Sequence 5, Application US/10124090
; Publication No. US20030171272A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Zcys7: A Member of the Cystatin
;  TITLE OF INVENTION:  Superfamily
;  FILE REFERENCE: 00-38
;  CURRENT APPLICATION NUMBER: US/10/124,090
;  CURRENT FILING DATE:  2002-04-16
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-10-124-090-5

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 59
US-10-124-090-6
; Sequence 6, Application US/10124090
; Publication No. US20030171272A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  TITLE OF INVENTION: Zcys7: A Member of the Cystatin
;  TITLE OF INVENTION:  Superfamily
;  FILE REFERENCE: 00-38
;  CURRENT APPLICATION NUMBER: US/10/124,090
;  CURRENT FILING DATE:  2002-04-16
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Illustrative nucleotide sequence.
US-10-124-090-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 60
US-10-277-494-134/c
; Sequence 134, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
;  TITLE OF INVENTION:  Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-K (400/064)
;  CURRENT APPLICATION NUMBER: US/10/277,494
;  CURRENT FILING DATE:  2002-10-21
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
;   LENGTH: 9
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-277-494-134

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GGAGCCC 14
              |||||||
Db          9 GGAGCCC 3


RESULT 61
US-10-277-494-212
; Sequence 212, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
;  TITLE OF INVENTION:  Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-K (400/064)
;  CURRENT APPLICATION NUMBER: US/10/277,494
;  CURRENT FILING DATE:  2002-10-21
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 212
;   LENGTH: 9
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-277-494-212

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GGAGCCC 14
              |||||||
Db          2 GGAGCCC 8


RESULT 62
```

US-10-152-363A-57/c
; Sequence 57, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Illustrative nucleotide sequence.
US-10-152-363A-57

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3
```

RESULT 63
US-10-152-363A-58
; Sequence 58, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Illustrative nucleotide sequence.
US-10-152-363A-58

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7
```

Search completed: November 17, 2003, 09:21:14
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 17, 2003, 09:10:59 ; Search time 0.001 Seconds
(without alignments)
19.960 Million cell updates/sec

Title: us-10-008-789-22
Perfect score: 20
Sequence: 1 gcttcagggagcccgtgcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 50 seqs, 499 residues

Total number of hits satisfying chosen parameters: 100

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : rge.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	10.4	52.0	13	1	AR002206	ACCESSION:AR002206
c	2	9.4	47.0	11	1	AX623720	ACCESSION:AX623720
	3	9.4	47.0	11	1	AX630279	ACCESSION:AX630279
c	4	9.4	47.0	11	1	AX631141	ACCESSION:AX631141
	5	9	45.0	10	1	AX152921	ACCESSION:AX152921
	6	9	45.0	10	1	AX538718	ACCESSION:AX538718
c	7	9	45.0	11	1	AX098793	ACCESSION:AX098793
	8	9	45.0	11	1	AX098794	ACCESSION:AX098794
c	9	9	45.0	11	1	AX470626	ACCESSION:AX470626
c	10	9	45.0	11	1	AX624031	ACCESSION:AX624031
c	11	9	45.0	11	1	AX631452	ACCESSION:AX631452
	12	8.4	42.0	10	1	AX152864	ACCESSION:AX152864
	13	8.4	42.0	10	1	AX152865	ACCESSION:AX152865
	14	8.4	42.0	10	1	BD007939	ACCESSION:BD007939
	15	8.4	42.0	10	1	BD083228	ACCESSION:BD083228
	16	8.4	42.0	11	1	AX099091	ACCESSION:AX099091
c	17	8.4	42.0	11	1	AX099092	ACCESSION:AX099092
c	18	8.4	42.0	11	1	AX471432	ACCESSION:AX471432
c	19	8.4	42.0	11	1	AX626821	ACCESSION:AX626821
c	20	8.4	42.0	11	1	AX626928	ACCESSION:AX626928
	21	8.4	42.0	11	1	AX627689	ACCESSION:AX627689
c	22	8.4	42.0	11	1	AX627862	ACCESSION:AX627862
c	23	8.4	42.0	11	1	AX629442	ACCESSION:AX629442
c	24	8	40.0	9	1	AX009053	ACCESSION:AX009053
c	25	8	40.0	10	1	AR162919	ACCESSION:AR162919
c	26	8	40.0	10	1	AX096928	ACCESSION:AX096928
	27	8	40.0	10	1	AX152540	ACCESSION:AX152540
c	28	8	40.0	10	1	AX152940	ACCESSION:AX152940
c	29	8	40.0	10	1	AX301376	ACCESSION:AX301376
c	30	8	40.0	10	1	BD166804	ACCESSION:BD166804
c	31	8	40.0	10	1	IS4931	ACCESSION:IS4931
	32	7.4	37.0	9	1	AX668683	ACCESSION:AX668683
	33	7.4	37.0	9	1	AX668684	ACCESSION:AX668684
	34	7.4	37.0	9	1	AX668685	ACCESSION:AX668685
	35	7.4	37.0	9	1	AX668686	ACCESSION:AX668686
	36	7.4	37.0	9	1	E12006	ACCESSION:E12006
c	37	7	35.0	9	1	AX318479	ACCESSION:AX318479
	38	7	35.0	9	1	AX318480	ACCESSION:AX318480
c	39	7	35.0	9	1	AX337949	ACCESSION:AX337949
	40	7	35.0	9	1	AX337950	ACCESSION:AX337950
c	41	7	35.0	9	1	AX337955	ACCESSION:AX337955
	42	7	35.0	9	1	AX337956	ACCESSION:AX337956
	43	7	35.0	9	1	AX668672	ACCESSION:AX668672
	44	7	35.0	9	1	AX668673	ACCESSION:AX668673
	45	7	35.0	9	1	AX668723	ACCESSION:AX668723
	46	7	35.0	9	1	AX668724	ACCESSION:AX668724
	47	7	35.0	9	1	AX668737	ACCESSION:AX668737
	48	7	35.0	9	1	AX668738	ACCESSION:AX668738
	49	7	35.0	9	1	AX668757	ACCESSION:AX668757
	50	7	35.0	9	1	AX668795	ACCESSION:AX668795

ALIGNMENTS

RESULT 1
AR002206/c
LOCUS AR002206 13 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 60 from patent US 5741490.
ACCESSION AR002206
VERSION AR002206.1 GI:3963760
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.D.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 5741490-A 60 21-APR-1998;
FEATURES Location/Qualifiers
source 1. .13
/organism="unknown"
BASE COUNT 1 a 7 c 3 g 2 t

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.9;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 TCAGGGAGCCCG 15
              ||||||||| ||
Db         13 TCAGGGAGCGCG 2
```

RESULT 2
AX623720/c
LOCUS AX623720 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 761 from Patent WO02053774.
ACCESSION AX623720
VERSION AX623720.1 GI:28451661
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 761 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 3 c 3 g 2 t

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  Query Match            47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity  90.9%;  Pred. No. 5.7;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGGAGC 12
              |||||| ||||
Db         11 CTTCAGTGAGC 1


RESULT 3
AX630279
LOCUS       AX630279                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7320 from Patent WO02053774.
ACCESSION   AX630279
VERSION     AX630279.1  GI:28458317
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7320 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      7 g      0 t

  Query Match            47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity  90.9%;  Pred. No. 5.7;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGTG 17
              ||||||||| |
Db          1 GGGAGCCCGGG 11


RESULT 4
AX631141/c
LOCUS       AX631141                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8182 from Patent WO02053774.
ACCESSION   AX631141
VERSION     AX631141.1  GI:28459185
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8182 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      3 g      2 t

  Query Match            47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity  90.9%;  Pred. No. 5.7;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGGAGC 12
              |||||| ||||
Db         11 CTTCAGTGAGC 1


RESULT 5
AX152921
LOCUS       AX152921                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 836 from Patent WO0138577.
ACCESSION   AX152921
VERSION     AX152921.1  GI:14534572
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 836 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      6 g      0 t

  Query Match            45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 7.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCG 15
              |||||||||
Db          1 GGGAGCCCG 9


RESULT 6
AX538718
LOCUS       AX538718                 10 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 10 from Patent WO02073212.
ACCESSION   AX538718
VERSION     AX538718.1  GI:25271343
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nagy,Z.
  TITLE     Diagnostic screens for alzheimer's disease
  JOURNAL   Patent: WO 02073212-A 10 19-SEP-2002;
            Isis Innovation Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="RAPD primer"
BASE COUNT        2 a      2 c      4 g      2 t

  Query Match            45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 7.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              |||||||||
Db          2 GCTTCAGGG 10


RESULT 7
AX098793/c
LOCUS       AX098793                 11 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 100 from Patent WO0120025.
ACCESSION   AX098793
VERSION     AX098793.1  GI:13538034
KEYWORDS    .
SOURCE      synthetic construct
```

```
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Eiselt,R.
  TITLE     Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
            diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0120025-A 100 22-MAR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial"
BASE COUNT        3 a      5 c      1 g      2 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGAG 11
              |||||||||
Db         10 TTCAGGGAG 2


RESULT 8
AX098794
LOCUS       AX098794                 11 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 101 from Patent WO0120025.
ACCESSION   AX098794
VERSION     AX098794.1  GI:13538035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Eiselt,R.
  TITLE     Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
            diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0120025-A 101 22-MAR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial"
BASE COUNT        2 a      1 c      5 g      3 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGAG 11
              |||||||||
Db          2 TTCAGGGAG 10


RESULT 9
AX470626/c
LOCUS       AX470626                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 203 from Patent WO02053773.
ACCESSION   AX470626
VERSION     AX470626.1  GI:22205751
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 203 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      2 g      2 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGAG 11
              |||||||||
Db          9 TTCAGGGAG 1


RESULT 10
AX624031/c
LOCUS       AX624031                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1072 from Patent WO02053774.
ACCESSION   AX624031
VERSION     AX624031.1  GI:28451972
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1072 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      2 g      2 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGAG 11
              |||||||||
Db          9 TTCAGGGAG 1


RESULT 11
AX631452/c
LOCUS       AX631452                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8494 from Patent WO02053774.
ACCESSION   AX631452
VERSION     AX631452.1  GI:28459518
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8494 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      2 g      2 t

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
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  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGAG 11
              |||||||||
Db          9 TTCAGGGAG 1


RESULT 12
AX152864
LOCUS       AX152864                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 779 from Patent WO0138577.
ACCESSION   AX152864
VERSION     AX152864.1  GI:14534515
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 779 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              |||||||| |
Db          1 GGGAGCCCCT 10


RESULT 13
AX152865
LOCUS       AX152865                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 780 from Patent WO0138577.
ACCESSION   AX152865
VERSION     AX152865.1  GI:14534516
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 780 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      4 g      1 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              |||||||| |
Db          1 GGGAGCCCCT 10


RESULT 14
BD007939
LOCUS       BD007939                 10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007939
VERSION     BD007939.1  GI:18636312
KEYWORDS    JP 2001069993-A/215.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 215 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/215
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      4 c      4 g      2 t

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 GAGCCCGTGC 18
              | ||||||||
Db          1 GTGCCCGTGC 10


RESULT 15
BD083228
LOCUS       BD083228                 10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human matured/activated dendritic cell expression genes.
ACCESSION   BD083228
VERSION     BD083228.1  GI:22628838
KEYWORDS    JP 2001327293-A/149.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
  TITLE     Human matured/activated dendritic cell expression genes
  JOURNAL   Patent: JP 2001327293-A 149 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001327293-A/149
            PD   27-NOV-2001
            PF   22-MAY-2000 JP 2000150562
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
              NAGAI
            PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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                    /db_xref="taxon:9606"
BASE COUNT        0 a      4 c      4 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 GAGCCCGTGC 18
              | ||||||||
Db          1 GTGCCCGTGC 10


RESULT 16
AX099091
LOCUS       AX099091                 11 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 154 from Patent WO0120026.
ACCESSION   AX099091
VERSION     AX099091.1  GI:13538301
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Hustert,E.
  TITLE     Polymorphisms in the human hpxr gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0120026-A 154 22-MAR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"
BASE COUNT        2 a      2 c      6 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              | ||||||||
Db          2 TGAGGGAGCC 11


RESULT 17
AX099092/c
LOCUS       AX099092                 11 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 155 from Patent WO0120026.
ACCESSION   AX099092
VERSION     AX099092.1  GI:13538302
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Hustert,E.
  TITLE     Polymorphisms in the human hpxr gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0120026-A 155 22-MAR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"
BASE COUNT        1 a      6 c      2 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              | ||||||||
Db         10 TGAGGGAGCC 1


RESULT 18
AX471432/c
LOCUS       AX471432                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1009 from Patent WO02053773.
ACCESSION   AX471432
VERSION     AX471432.1  GI:22206557
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1009 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      5 c      5 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              ||||| ||||
Db         10 CAGGGGGCCC 1


RESULT 19
AX626821/c
LOCUS       AX626821                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3862 from Patent WO02053774.
ACCESSION   AX626821
VERSION     AX626821.1  GI:28454859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3862 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      2 g      3 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGGAG 11
              | ||||||||
Db         11 CATCAGGGAG 2


RESULT 20
AX626928/c
LOCUS       AX626928                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3969 from Patent WO02053774.
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ACCESSION   AX626928
VERSION     AX626928.1  GI:28454966
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3969 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      5 c      5 g      1 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              ||||| ||||
Db         10 CAGGGGGCCC 1


RESULT 21
AX627689
LOCUS       AX627689                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4730 from Patent WO02053774.
ACCESSION   AX627689
VERSION     AX627689.1  GI:28455727
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4730 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      5 g      0 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              |||||||| |
Db          1 CAGGGAGCGC 10


RESULT 22
AX627862/c
LOCUS       AX627862                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4903 from Patent WO02053774.
ACCESSION   AX627862
VERSION     AX627862.1  GI:28455900
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4903 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      6 c      2 g      2 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GGAGCCCGTG 17
              ||||| ||||
Db         11 GGAGCGCGTG 2


RESULT 23
AX629442/c
LOCUS       AX629442                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6483 from Patent WO02053774.
ACCESSION   AX629442
VERSION     AX629442.1  GI:28457480
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6483 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      4 g      3 t

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              ||| ||||||
Db         10 TCAAGGAGCC 1


RESULT 24
AX009053/c
LOCUS       AX009053                   9 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 86 from Patent WO9963975.
ACCESSION   AX009053
VERSION     AX009053.1  GI:9996427
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
  TITLE     A method for stimulating the immune system
  JOURNAL   Patent: WO 9963975-A 86 16-DEC-1999;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
            HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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BASE COUNT        0 a      4 c      4 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GGAGCCCG 15
              ||||||||
Db          8 GGAGCCCG 1


RESULT 25
AR162919/c
LOCUS       AR162919                  10 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6260034.
ACCESSION   AR162919
VERSION     AR162919.1  GI:16230279
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Bjorkesten,L.
  TITLE     Method and a system for nucleic acid sequence analysis
  JOURNAL   Patent: US 6260034-A 1 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        2 a      4 c      2 g      2 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGG 8
              ||||||||
Db          8 GCTTCAGG 1


RESULT 26
AX096928/c
LOCUS       AX096928                  10 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 2106 from Patent WO0118250.
ACCESSION   AX096928
VERSION     AX096928.1  GI:13513196
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 2106 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      4 c      2 g      3 t      1 others

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGC 12
              ||||||||
Db          9 CAGGGAGC 2


RESULT 27
AX152540
LOCUS       AX152540                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 455 from Patent WO0138577.
ACCESSION   AX152540
VERSION     AX152540.1  GI:14534191
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 455 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      3 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GCCCGTGC 18
              ||||||||
Db          1 GCCCGTGC 8


RESULT 28
AX152940/c
LOCUS       AX152940                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 855 from Patent WO0138577.
ACCESSION   AX152940
VERSION     AX152940.1  GI:14534591
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 855 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      5 c      1 g      3 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAG 11
              ||||||||
Db          9 TCAGGGAG 2


RESULT 29
AX301376/c
LOCUS       AX301376                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 90 from Patent WO0185941.
ACCESSION   AX301376
VERSION     AX301376.1  GI:17382459
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 90 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      2 g      3 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGC 12
              ||||||||
Db         10 CAGGGAGC 3


RESULT 30
BD166804/c
LOCUS       BD166804                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166804
VERSION     BD166804.1  GI:27872616
KEYWORDS    JP 2002209591-A/349.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 349 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/349
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      3 c      3 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGG 9
              ||||||||
Db          8 CTTCAGGG 1


RESULT 31
I54931/c
LOCUS       I54931                   10 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 21 from patent US 5646126.
ACCESSION   I54931
VERSION     I54931.1  GI:2476134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Cheng,Y.-c., Lukhtanov,E.A., Meyer,R.B. Jr., Pai,B.S., Reed,M.W.
            and Zhou,J.H.
  TITLE     Sterol modified oligonucleotide duplexes having anticancer activity
  JOURNAL   Patent: US 5646126-A 21 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        1 a      3 c      5 g      1 t

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGCG 19
               ||||||||
Db          8 CCCGTGCG 1


RESULT 32
AX668683
LOCUS       AX668683                 9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2132 from Patent WO0242459.
ACCESSION   AX668683
VERSION     AX668683.1  GI:29291658
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2132 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      5 g      1 t

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 33
AX668684
LOCUS       AX668684                 9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2133 from Patent WO0242459.
ACCESSION   AX668684
VERSION     AX668684.1  GI:29291659
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2133 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
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     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      5 g      1 t

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 34
AX668685
LOCUS       AX668685                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2134 from Patent WO0242459.
ACCESSION   AX668685
VERSION     AX668685.1  GI:29291660
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2134 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      5 g      1 t

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 35
AX668686
LOCUS       AX668686                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2135 from Patent WO0242459.
ACCESSION   AX668686
VERSION     AX668686.1  GI:29291661
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2135 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      5 g      1 t

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9


RESULT 36
E12006
LOCUS       E12006                    9 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Primer.
ACCESSION   E12006
VERSION     E12006.1  GI:22027434
KEYWORDS    JP 1996228799-A/21.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Onda,H. and Hosoya,M.
  TITLE     DNA PRIMER AND SCREENING OF DNA
  JOURNAL   Patent: JP 1996228799-A 21 10-SEP-1996;
            TAKEDA CHEM IND LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996228799-A/21
            PD   10-SEP-1996
            PF   04-DEC-1995 JP 1995337716
            PR   05-DEC-1994 JP 94P   300657
            PI   ONDA HARUO, HOSOYA MASAKI
            PC   C12Q1/68,C07H21/04,C07K14/575,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .9
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      3 c      3 g      1 t

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCC 13
              || ||||||
Db          1 CATGGAGCC 9


RESULT 37
AX318479/c
LOCUS       AX318479                  9 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 1 from Patent WO0181596.
ACCESSION   AX318479
VERSION     AX318479.1  GI:17900940
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lok,S.
  TITLE     Methods for enhancing the expression of a protein of interest by
            recombinant host cells
  JOURNAL   Patent: WO 0181596-A 1 01-NOV-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Illustrative nucleotide sequence."
BASE COUNT        2 a      2 c      4 g      1 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 38
AX318480
LOCUS       AX318480                   9 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 2 from Patent WO0181596.
ACCESSION   AX318480
VERSION     AX318480.1  GI:17900941
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lok,S.
  TITLE     Methods for enhancing the expression of a protein of interest by
            recombinant host cells
  JOURNAL   Patent: WO 0181596-A 2 01-NOV-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Illustrative nucleotide sequence."
BASE COUNT        1 a      4 c      2 g      2 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 39
AX337949/c
LOCUS       AX337949                   9 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 5 from Patent WO0194389.
ACCESSION   AX337949
VERSION     AX337949.1  GI:18128667
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R. and Gao,Z.
  TITLE     Zcys7: a member of the cystatin superfamily
  JOURNAL   Patent: WO 0194389-A 5 13-DEC-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Illustrative nucleotide sequence."
BASE COUNT        2 a      2 c      4 g      1 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 40
AX337950
LOCUS       AX337950                   9 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 6 from Patent WO0194389.
ACCESSION   AX337950
VERSION     AX337950.1  GI:18128668
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R. and Gao,Z.
  TITLE     Zcys7: a member of the cystatin superfamily
  JOURNAL   Patent: WO 0194389-A 6 13-DEC-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Illustrative nucleotide sequence."
BASE COUNT        1 a      4 c      2 g      2 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          1 CCCGTGC 7


RESULT 41
AX337955/c
LOCUS       AX337955                   9 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 5 from Patent WO0194388.
ACCESSION   AX337955
VERSION     AX337955.1  GI:18128672
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R. and Gao,Z.
  TITLE     Zcys6: a member of the cystatin superfamily
 .JOURNAL   Patent: WO 0194388-A 5 13-DEC-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Illustrative nucleotide sequence."
BASE COUNT        2 a      2 c      4 g      1 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


RESULT 42
AX337956
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LOCUS       AX337956                  9 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 6 from Patent WO0194388.
ACCESSION   AX337956
VERSION     AX337956.1  GI:18128673
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R. and Gao,Z.
  TITLE     Zcys6: a member of the cystatin superfamily
  JOURNAL   Patent: WO 0194388-A 6 13-DEC-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Illustrative nucleotide sequence."
BASE COUNT        1 a      4 c      2 g      2 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CCCGTGC 18
               |||||||
Db           1 CCCGTGC 7


RESULT 43
AX668672
LOCUS       AX668672                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2121 from Patent WO0242459.
ACCESSION   AX668672
VERSION     AX668672.1  GI:29291647
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2121 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        3 a      1 c      5 g      0 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
               |||||||
Db          1 CAGGGAG 7


RESULT 44
AX668673
LOCUS       AX668673                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2122 from Patent WO0242459.
ACCESSION   AX668673
VERSION     AX668673.1  GI:29291648
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2122 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        3 a      1 c      5 g      0 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
               |||||||
Db          1 CAGGGAG 7


RESULT 45
AX668723
LOCUS       AX668723                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2172 from Patent WO0242459.
ACCESSION   AX668723
VERSION     AX668723.1  GI:29291698
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2172 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      6 g      0 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
               |||||||
Db          3 GGGAGCC 9


RESULT 46
AX668724
LOCUS       AX668724                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2173 from Patent WO0242459.
ACCESSION   AX668724
VERSION     AX668724.1  GI:29291699
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2173 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
```

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    source          1. .9
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
                    /note="example target DNA"
BASE COUNT        1 a      2 c      6 g      0 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 47
AX668737
LOCUS       AX668737                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2186 from Patent WO0242459.
ACCESSION   AX668737
VERSION     AX668737.1  GI:29291712
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2186 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        2 a      2 c      5 g      0 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 48
AX668738
LOCUS       AX668738                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2187 from Patent WO0242459.
ACCESSION   AX668738
VERSION     AX668738.1  GI:29291713
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2187 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        2 a      2 c      5 g      0 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 49
AX668757
LOCUS       AX668757                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2206 from Patent WO0242459.
ACCESSION   AX668757
VERSION     AX668757.1  GI:29291732
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2206 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      5 g      1 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 50
AX668795
LOCUS       AX668795                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2244 from Patent WO0242459.
ACCESSION   AX668795
VERSION     AX668795.1  GI:29291770
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2244 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"
BASE COUNT        1 a      2 c      5 g      1 t

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9
```

Search completed: November 17, 2003, 09:11:00
Job time : 1 secs

OM nucleic - nucleic search, using sw model

Run on: November 17, 2003, 09:12:51 ; Search time 0.001 Seconds
(without alignments)
45.200 Million cell updates/sec

Title: us-10-008-789-22
Perfect score: 20
Sequence: 1 gcttcagggagcccgtgcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 114 seqs, 1130 residues

Total number of hits satisfying chosen parameters: 228

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 114 summaries

Database : rng.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	11.8	59.0	15	1	AAF50238	IGF-I oligonucleot
	2	11.8	59.0	15	1	AAS98729	Colony stimulating
	3	10.4	52.0	13	1	AAV11102	Human ribozyme tar
c	4	10	50.0	10	1	AAZ82409	Metastatic breast
	5	10	50.0	12	1	AAA52398	TdT-expressing Ram
c	6	9.4	47.0	11	1	ABV62975	Human skin EST 761
	7	9.4	47.0	11	1	ABV69534	Human skin EST 732
c	8	9.4	47.0	11	1	ABV70396	Human skin EST 818
	9	9	45.0	10	1	AAZ78197	Human dendritic ce
	10	9	45.0	10	1	AAZ82165	Metastatic breast
	11	9	45.0	10	1	AAS57281	Human CHRNB2 allel
	12	9	45.0	10	1	AAH63996	Human ubiquitously
	13	9	45.0	10	1	ABV73322	Somatic mutation s
c	14	9	45.0	10	1	AAD47781	Human GNB3 gene po
c	15	9	45.0	11	1	AAS01932	Cytochrome P-450 (
	16	9	45.0	11	1	AAS01933	Cytochrome P-450 (
c	17	9	45.0	11	1	ABV63286	Human skin EST 107
c	18	9	45.0	11	1	ABV70707	Human skin EST 849
c	19	9	45.0	11	1	ABQ86448	Human skin stress/
	20	9	45.0	12	1	ABK72572	Human OPA1 gene, e
	21	8.4	42.0	10	1	AAA56517	Human macrophage g
	22	8.4	42.0	10	1	AAA14247	Camel male-associa
c	23	8.4	42.0	10	1	AAZ78376	Human dendritic ce
c	24	8.4	42.0	10	1	AAZ81654	Metastatic breast
	25	8.4	42.0	10	1	AAZ82050	Metastatic breast
	26	8.4	42.0	10	1	AAZ83201	Metastatic breast
	27	8.4	42.0	10	1	AAZ84054	Metastatic breast
c	28	8.4	42.0	10	1	AAZ84542	Metastatic breast
	29	8.4	42.0	10	1	AAZ85030	Metastatic breast
	30	8.4	42.0	10	1	AAZ85257	Metastatic breast
	31	8.4	42.0	10	1	AAZ85646	Metastatic breast
c	32	8.4	42.0	10	1	AAZ85771	Metastatic breast
	33	8.4	42.0	10	1	AAH63939	Human ubiquitously
	34	8.4	42.0	10	1	AAH63940	Human ubiquitously
	35	8.4	42.0	10	1	AAH20558	Human MTR1 exon14/
	36	8.4	42.0	10	1	AAH32842	LPS activated huma
	37	8.4	42.0	10	1	AAF75023	HTR1A gene polymor
c	38	8.4	42.0	10	1	AAF40219	Yeast NORF gene SA
	39	8.4	42.0	10	1	AAF42414	Yeast NORF gene SA
c	40	8.4	42.0	10	1	AAL48143	Human neuropeptide
	41	8.4	42.0	10	1	ABK81799	Human CHRM5 gene p
	42	8.4	42.0	10	1	AAS98841	Colony stimulating
	43	8.4	42.0	10	1	AAD25027	Human AANAT gene p
	44	8.4	42.0	10	1	ABL42775	Human maturation/a
	45	8.4	42.0	10	1	ABT14329	Nucleic acid PCR a
c	46	8.4	42.0	11	1	AAQ51997	B-cell mRNA ribozy
	47	8.4	42.0	11	1	AAS02884	Human pregnane X r
c	48	8.4	42.0	11	1	AAS02885	Human pregnane X r
c	49	8.4	42.0	11	1	ABV66076	Human skin EST 386
c	50	8.4	42.0	11	1	ABV66183	Human skin EST 396
	51	8.4	42.0	11	1	ABV66944	Human skin EST 473
c	52	8.4	42.0	11	1	ABV67117	Human skin EST 490
c	53	8.4	42.0	11	1	ABV68697	Human skin EST 648
c	54	8.4	42.0	11	1	ABQ87254	Human skin stress/
c	55	8.4	42.0	11	1	ABL51577	Transferrin recept
c	56	8	40.0	8	1	AAT09422	5'-primer used for
	57	8	40.0	8	1	AAT09561	3'-primer used for
c	58	8	40.0	9	1	AAZ65526	Immunosuppressant
c	59	8	40.0	10	1	AAX32621	Anticancer duplex
c	60	8	40.0	10	1	AAZ80768	Metastatic breast
c	61	8	40.0	10	1	AAZ82243	Metastatic breast
	62	8	40.0	10	1	AAZ82499	Metastatic breast
	63	8	40.0	10	1	AAZ83879	Metastatic breast
c	64	8	40.0	10	1	AAZ85236	Metastatic breast
	65	8	40.0	10	1	AAZ85403	Metastatic breast
	66	8	40.0	10	1	AAZ85929	Metastatic breast
	67	8	40.0	10	1	AAH63615	Human ubiquitously
c	68	8	40.0	10	1	AAH64015	Human ubiquitously
c	69	8	40.0	10	1	AAF97341	Human gene single
c	70	8	40.0	10	1	AAF37906	Yeast NORF gene SA
c	71	8	40.0	10	1	AAF42841	Yeast NORF gene SA
c	72	8	40.0	10	1	AAD44471	Human F2RL1 gene p
c	73	8	40.0	10	1	ABV84539	Human cDNA clone P
	74	8	40.0	10	1	ABT05343	Human NAGA-alpha g
c	75	8	40.0	10	1	ABK96539	Human PLAU gene, p
c	76	8	40.0	10	1	ABK85687	Human SCYB6 gene p
	77	8	40.0	10	1	ABA98387	SCN2B gene polymor
	78	8	40.0	10	1	ABK70549	Human G protein-co
c	79	8	40.0	10	1	ABL52211	Human PER1 preferr
c	80	8	40.0	10	1	ABL52257	Human PHKG2 prefer
c	81	8	40.0	10	1	ABK23463	Transcript tag DNA
	82	8	40.0	10	1	AAD26187	Human endothelin 2
	83	8	40.0	10	1	AAS19975	Primer-extension o
	84	8	40.0	10	1	ABL39540	Human ETFB primer-
	85	8	40.0	10	1	ABT14248	Nucleic acid PCR a
	86	7.4	37.0	9	1	AAX54701	Muscarinic acetylc
	87	7.4	37.0	9	1	AAF20270	Human muscarinic a
	88	7.4	37.0	9	1	AAA34148	Human adenosine re
	89	7.4	37.0	9	1	ABQ71834	Zinc finger protei
	90	7.4	37.0	9	1	ABQ71835	Zinc finger protei
	91	7.4	37.0	9	1	ABQ71836	Zinc finger protei
	92	7.4	37.0	9	1	ABQ71837	Zinc finger protei
	93	7	35.0	8	1	AAT09588	3'-primer used for
c	94	7	35.0	8	1	AAT09371	5'-primer used for
c	95	7	35.0	8	1	AAT09466	5'-primer used for
c	96	7	35.0	8	1	AAT09425	5'-primer used for
	97	7	35.0	8	1	AAT09562	3'-primer used for
	98	7	35.0	8	1	AAT09544	3'-primer used for
	99	7	35.0	8	1	AAX78349	Electrochemical de
c	100	7	35.0	8	1	AAX29509	Primer for human n
	101	7	35.0	8	1	AAA80773	A. thaliana primer
c	102	7	35.0	8	1	AAA81033	A. thaliana primer
c	103	7	35.0	8	1	AAA81034	A. thaliana primer
	104	7	35.0	9	1	AAQ37100	Phoma lingam patho
c	105	7	35.0	9	1	AAT27993	Monoclonal antibod
	106	7	35.0	9	1	ABQ71823	Zinc finger protei

107	7	35.0	9	1	ABQ71824	Zinc finger protei
108	7	35.0	9	1	ABQ71874	Zinc finger protei
109	7	35.0	9	1	ABQ71875	Zinc finger protei
110	7	35.0	9	1	ABQ71888	Zinc finger protei
111	7	35.0	9	1	ABQ71889	Zinc finger protei
112	7	35.0	9	1	ABQ71908	Zinc finger protei
113	7	35.0	9	1	ABQ71946	Zinc finger protei
c 114	7	35.0	9	1	AAD53774	TACI related oligo

ALIGNMENTS

RESULT 1
AAF50238/c
ID AAF50238 standard; DNA; 15 BP.
XX
AC AAF50238;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #1198.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU00693.
XX
PR 21-JUN-1999; 99US-0140345.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
PS Example 8; Page 68; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-F45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
SQ Sequence 15 BP; 4 A; 3 C; 6 G; 2 T; 0 other;

Query Match 59.0%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 4.8;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 CTTCAGGGAGCCCGT 16
              ||||| | |||||||
Db         15 CTTCACGTAGCCCGT 1
```

RESULT 2
AAS98729
ID AAS98729 standard; DNA; 15 BP.
XX
AC AAS98729;
XX
DT 26-MAR-2002 (first entry)
XX
DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #95.
XX
KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW cytostatic; gene therapy; malignant histiocytosis; isogene;
KW myeloid malignancy; inflammatory disorder; transgenic animal;
KW haplotype; genotype; human; allele specific oligonucleotide; ASO;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200179225-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US12044.
XX
PR 12-APR-2000; 2000US-196411P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075058/10.
XX
PT Novel polymorphic variants of colony stimulating factor 1 receptor
PT useful in studying expression and function of the protein, useful for
PT screening candidate drugs to treat diseases e.g. inflammatory disorders
PT -
XX
PS Claim 15; Page 16; 164pp; English.
XX
CC The invention describes a novel isolated polynucleotide (I) comprising a
CC sequence which is a polymorphic variant (PV) of a reference sequence for
CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
CC polypeptide are useful for improving the discovery and development of
CC drugs for treating diseases associated with CSF1R activity, e.g.,
CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
CC and the haplotypes can be used to validate CSF1R as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
CC be used in developing diagnostic tests and therapeutic treatments. (I) is
CC useful in studying the expression and function of CSF1R, and in
CC expressing CSF1R protein for use in screening for candidate drugs to
CC treat diseases related to CSF1R activity and in studying the effect of
CC the variation on the biological activity of CSF1R as well as on the
CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
CC useful in a variety of diagnostic and prognostic formats and therapeutic
CC methods. A transgenic animal is useful in studying expression of the
CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against CSF1R protein, and for testing the efficacy of
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC are useful as probes and primers, and for assaying a polymorphism in the
CC target region. Without requiring any a priori knowledge of the phenotypic
CC effect of any particular CSF1R or haplotype the invention provides a
CC method for identifying lead compounds that are more likely to show
CC efficacy in clinical trials. This sequence is an allele specific

```
CC   oligonucleotide primer used for detecting CSF1R gene polymorphisms,
CC   described in the method of the invention.
XX
SQ   Sequence 15 BP; 2 A; 3 C; 6 G; 3 T; 1 other;

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.8;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGAGCCCGTG 17
              ||||||||||| | |
Db          1 TTCAGGGAGCCTGRG 15


RESULT 3
AAV11102
ID   AAV11102 standard; RNA; 13 BP.
XX
AC   AAV11102;
XX
DT   25-MAR-2003  (updated)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DRB 11DRB #1.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP03173.
XX
PR   18-JUL-1995;   95EP-0111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to
PT   treat auto:immune disease
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a
CC   specific family of closely related MHC alleles or to mRNA from a single
CC   MHC allele, and is able to cleave such mRNA. The mRNA has a target
CC   region which in case is essentially conserved in all genes of the family
CC   but differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This
CC   allows the selective reduction or inhibition of expression of all genes
CC   of a family or of a single gene. This ribozyme can be used for permanent
CC   or transient suppression of expression of MHC alleles, in vivo or in
CC   vitro. Specific applications are to prevent guest vs. host or host vs.
CC   guest reactions, to prevent blood incompatibilities (partic. of the ABO,
CC   rhesus and Kell systems) and to treat autoimmune diseases such as
CC   juvenile diabetes and rheumatoid arthritis. The use of this ribozyme
CC   avoids the need for immunosuppressants in transplant patients. It
CC   provides very specific reduction of particular HLA molecules that cause
CC   incompatibility between donor and recipient.
CC   (Updated on 25-MAR-2003 to correct PA field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 2 A; 3 C; 6 G; 2 U; 0 other;

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 11;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GGAGCCCGTGCG 19
              |||| |||:|||
Db          2 GGAGUCCGUGCG 13


RESULT 4
AAZ82409/c
ID   AAZ82409 standard; DNA; 10 BP.
XX
AC   AAZ82409;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1643.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 102; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
```

```
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              ||||||||||
Db         10 TCAGGGAGCC 1


RESULT 5
AAA52398
ID   AAA52398 standard; DNA; 12 BP.
XX
AC   AAA52398;
XX
DT   18-SEP-2000  (first entry)
XX
DE   TdT-expressing Ramos cell VH deletion mutation, F66.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; heavy chain variable region; VH;
KW   mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-GB03358.
XX
PR   09-OCT-1998;   98GB-0022104.
PR   19-JAN-1999;   99GB-0001141.
PR   09-JUN-1999;   99GB-0013435.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Sale JE,  Neuberger MS,  Cumbers SJ;
XX
DR   WPI; 2000-317971/27.
XX
PT   Lymphoid cell line preparation useful for producing gene products
PT   having desired activity, involves screening and selecting cells having
PT   ongoing target sequence diversification and higher mutation rates  -
XX
PS   Example 4; Fig 6; 69pp; English.
XX
CC   The invention relates to a method of preparing a lymphoid cell line
CC   capable of capable of directed constitutive hypermutation of a target
CC   nucleic acid region. The method comprises screening a cell population
CC   for ongoing target sequence diversification and selecting a cell in which
CC   the rate of target nucleic acid mutation exceeds that of other nucleic
CC   acid mutation by a factor of 100 or more. The invention also relates to
CC   a method for preparing a gene product with a desired activity,
CC   comprising expressing a nucleic acid encoding the target gene operably
CC   linked to a sequence which directs hypermutation e.g., terminal
CC   deoxynucleotidyl transferase (TdT), in the lymphoid cell line, and
CC   identifying a cell or cells which express a mutated gene product with the
CC   desired activity. One or more clonal populations of the identified cells
CC   is established, and cells with an improved activity of interest are
CC   selected. These steps may be iteratively repeated until a gene product
CC   with a desired of activity is obtained. The cell lines prepared according
CC   to the method of the invention are used for directed constitutive
CC   hypermutation of a nucleic acid region in the preparation of a gene
CC   product, preferably an enzyme or an immunoglobulin (Ig) with a desired
CC   activity. In the exemplifications of the invention, IgM-secreting Ramos
CC   cells were selected for use as they undergo hypermutation during clonal
CC   expansion. This was determined on the basis of the amount of diversity in
CC   the heavy chain variable region (VH). Sequences AAA52366-A52434 represent
CC   fragments of Ramos cell VH region DNA containing mutations other than
CC   single nucleotide substitutions. The number assigned to the mutation
CC   represents the position in the wild-type VH DNA (AAA52364) to which the
CC   first nucleotide in the mutant fragment corresponds. Sequences
CC   AAA52388-A52434 represent mutations that occur in Ramos cells which
CC   express TdT, and sequences AAA52366-A52487 represent mutations that occur
CC   in non-TdT- expressing control Ramos cells.
XX
SQ   Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGGAG 11
              ||||||||||
Db          1 CTTCAGGGAG 10


RESULT 6
ABV62975/c
ID   ABV62975 standard; cDNA; 11 BP.
XX
AC   ABV62975;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 761.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 46; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
```

```
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 20;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGGAGC 12
              |||||| ||||
Db         11 CTTCAGTGAGC 1


RESULT 7
ABV69534
ID   ABV69534 standard; cDNA; 11 BP.
XX
AC   ABV69534;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7320.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 229; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 3 C; 7 G; 0 U; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 20;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGTG 17
              ||||||||| |
Db          1 GGGAGCCCGGG 11


RESULT 8
ABV70396/c
ID   ABV70396 standard; cDNA; 11 BP.
XX
AC   ABV70396;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8182.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Claim 24; Page 261; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 20;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGGAGC 12
              |||||| ||||
Db         11 CTTCAGTGAGC 1


RESULT 9
AAZ78197
ID   AAZ78197 standard; DNA; 10 BP.
XX
AC   AAZ78197;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:625.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
```

```
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13800.
XX
PR   19-JUN-1998;   98US-0089833.
PR   19-JUN-1998;   98US-0089844.
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089878.
PR   19-JUN-1998;   98US-0089991.
PR   19-JUN-1998;   98US-0089992.
PR   19-JUN-1998;   98US-0089993.
PR   19-JUN-1998;   98US-0089994.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0089999.
PR   19-JUN-1998;   98US-0090000.
PR   19-JUN-1998;   98US-0090035.
PR   19-JUN-1998;   98US-0090036.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
PR   19-JUN-1998;   98US-0090042.
PR   19-JUN-1998;   98US-0090043.
PR   19-JUN-1998;   98US-0090044.
PR   19-JUN-1998;   98US-0090045.
PR   19-JUN-1998;   98US-0090047.
PR   19-JUN-1998;   98US-0090048.
PR   19-JUN-1998;   98US-0090072.
PR   19-JUN-1998;   98US-0090076.
PR   19-JUN-1998;   98US-0090077.
PR   19-JUN-1998;   98US-0090078.
PR   19-JUN-1998;   98US-0090079.
PR   19-JUN-1998;   98US-0090080.
PR   08-DEC-1998;   98US-0111715.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer -
XX
PS   Claim 1; Page 83; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or
CC   ESTs (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can
CC   lyse the tumour cells, immunostimulatory cofactors also being required
CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell
CC   differentially expressed genes, or of their encoded proteins, can be used
CC   to identify cells as belonging to the monocyte lineage. Cells containing
CC   these genes can be used in active immunotherapy (or to stimulate
CC   production of a population of antigen-specific effector cells) and
CC   vectors containing them are used in gene therapy. Co-administration of
CC   tumour antigens and APC-associated costimulatory factors ensures adequate
CC   antigen presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 6 G; 0 U; 0 other;

  Query Match           45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCG 15
              |||||||||
Db          1 GGGAGCCCG 9


RESULT 10
AAZ82165
ID   AAZ82165 standard; DNA; 10 BP.
XX
AC   AAZ82165;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1399.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 96; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
```

```
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 6 G; 0 U; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCG 15
              |||||||||
Db          1 GGGAGCCCG 9


RESULT 11
AAS57281
ID   AAS57281 standard; DNA; 10 BP.
XX
AC   AAS57281;
XX
DT   16-JAN-2002  (first entry)
XX
DE   Human CHRNB2 allele specific oligonucleotide PCR primer terminus #6.
XX
KW   Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;
KW   CHRNB2; memory disorder; Alzheimer's disease; epilepsy; learning;
KW   chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;
KW   ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADNFLE; ss;
KW   allele specific oligonucleotide; ASO; PCR primer.
XX
OS   Homo sapiens.
XX
PN   WO200174833-A2.
XX
PD   11-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US10666.
XX
PR   03-APR-2000; 2000US-194155P.
PR   13-JUL-2000; 2000US-217952P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Kliem SE,  Koshy B,  Lee HH,  Sanchis A;
XX
DR   WPI; 2001-626374/72.
XX
PT   Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of
PT   an individual involves determining for two copies of the gene, the
PT   identity of nucleotide pair at polymorphic sites selected from PS1-24
PT   -
XX
PS   Claim 17; Page 15; 82pp; English.
XX
CC   The invention relates to genotyping/haplotyping the cholinergic receptor,
CC   nicotinic, beta-polypeptide 2 (neuronal) (CHRNB2) gene of an individual,
CC   comprising determining for the two copies of the CHRNB2 gene present in
CC   the individual, the identity of the nucleotide pair at one or more
CC   polymorphic sites selected from PS1-24. Also include are oligonucleotides
CC   for performing the method and the nucleotide sequence of the polymorphic
CC   variants of CHRNB2. The method is useful for detecting novel CHRNB2
CC   polymorphisms and for determining if an individual has a haplotype or
CC   haplotype pairs defined in the specification and to validate CHRNB2 as a
CC   candidate agent for treating a specific condition or disease predicted to
CC   be associated with CHRNB2 activity (e.g. a memory disorder, Alzheimer's
CC   disease, epilepsy, a learning disorder, schizophrenia, attention
CC   deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal
CC   frontal lobe epilepsy (ADNFLE)), and in the design of clinical trials
CC   of candidate drugs for treating a specific condition or disease
CC   predicted to be associated with CHRNB2 activity. The method is useful to
CC   screen for compounds targeting CHRNB2 to treat a specific conditions or
CC   disease associated with CHRNB2 activity. The polymorphic nucleic acids
CC   are useful in studying the expression and function of CHRNB2, and in
CC   expressing CHRNB2 protein for use in screening for candidate drugs to
CC   treat diseases related to CHRNB2 activity and are useful for therapeutic
CC   purposes. The CHRNB2 gene is located on chromosome 1q21. The present
CC   sequence is an allele specific oligonucleotide (ASO) PCR primer (3'
CC   terminus) for performing the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGC 12
              |||||||||
Db          2 TCAGGGAGC 10


RESULT 12
AAH63996
ID   AAH63996 standard; cDNA; 10 BP.
XX
AC   AAH63996;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 836.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 58; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
```

```
SQ   Sequence 10 BP; 1 A; 3 C; 6 G; 0 U; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCG 15
              |||||||||
Db          1 GGGAGCCCG 9


RESULT 13
ABV73322
ID   ABV73322 standard; DNA; 10 BP.
XX
AC   ABV73322;
XX
DT   22-JAN-2003  (first entry)
XX
DE   Somatic mutation screening RAPD primer.
XX
KW   Alzheimer's disease; cell cycle regulation; G1/S phase; mutation;
KW   genetic fingerprinting; RAPD; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200273212-A2.
XX
PD   19-SEP-2002.
XX
PF   12-MAR-2002; 2002WO-GB01137.
XX
PR   12-MAR-2001; 2001GB-0006051.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Nagy Z;
XX
DR   WPI; 2002-759852/82.
XX
PT   Diagnosing Alzheimer's disease (AD), particularly sporadic and familial
PT   AD, or predisposition to AD, comprises detecting a cell cycle
PT   regulatory defect at the G1/S phase transition in non-neuronal cells of
PT   the subject  -
XX
PS   Example 3; Page 33; 51pp; English.
XX
CC   The invention relates to diagnosing Alzheimer's disease (AD) in a human
CC   subject by screening for the presence of a cell cycle regulatory defect
CC   at the G1/S phase transition in non-neuronal cells of the subject. The
CC   method is useful for diagnosing Alzheimer's disease particularly sporadic
CC   AD and familial AD, or predisposition to AD. The diagnostic tests may
CC   also be applied in the development of animal models of early AD, e.g. for
CC   the identification of a mouse model which exhibits an analogous defect in
CC   cell cycle regulation to that present in AD. Sequences ABV73319-328
CC   represent short RAPD primers used to randomly amplify polymorphic DNA
CC   sequences, to screen for somatic mutations in neurons.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              |||||||||
Db          2 GCTTCAGGG 10


RESULT 14
AAD47781/c
ID   AAD47781 standard; DNA; 10 BP.
XX
AC   AAD47781;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human GNB3 gene polymorphisms detecting primer #1.
XX
KW   Human; guanine nucleotide binding protein beta polypeptide 3; G protein;
KW   GNB3; polymorphism; obesity; left ventricular hypertrophy; hypertension;
KW   drug discovery; cardiovascular; development process; asthma; anorectic;
KW   gene therapy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200277284-A1.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2001; 2001WO-US08961.
XX
PR   21-MAR-2001; 2001WO-US08961.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Choi JY,  Kliem SE,  Koshy B;
XX
DR   WPI; 2003-018947/01.
XX
PT   New genetic variants having polymorphisms in the G protein, GNB3 gene,
PT   useful for treating disorders with abnormal expression or function of
PT   the GNB3 gene, such as asthma, obesity, hypertension and left
PT   ventricular hypertrophy  -
XX
PS   Claim 18; Page 15; 88pp; English.
XX
CC   The invention relates to an isolated polypeptide which comprises a first
CC   nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for the guanine nucleotide binding protein (G protein), beta
CC   polypeptide 3 (GNB3) gene or fragment. Polymorphic variants of the GNB3
CC   gene are useful in studying the expression and biological function of
CC   GNB3 and in identifying drugs targetting GNB3 protein for treating
CC   disorders associated with abnormal expression or function of GNB3, e.g.
CC   hypertension, obesity, asthma and left ventricular hypertrophy.
CC   Polynucleotides comprising a polymorphic gene variant or fragment may be
CC   used for therapeutic purposes, where a patient could benefit from
CC   expression or increased expression of a particular GNB3 gene isoform or
CC   an expression vector encoding the isoform may be administered to the
CC   patient. Haplotype information is useful in improving the efficiency and
CC   output of several steps in drug discovery and development process,
CC   including target validation, identifying lead compounds and early phase
CC   clinical trials. The invention is used in gene therapy. The present
CC   sequence is human GNB3 gene polymorphisms detecting primer.
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGAG 11
              |||||||||
Db          9 TTCAGGGAG 1


RESULT 15
AAS01932/c
ID   AAS01932 standard; DNA; 11 BP.
XX
AC   AAS01932;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Cytochrome P-450 (CYP)3A4 gene exon 11 sense strand DNA #4.
XX
```

KW CYP3A4; CYP3A7; human; exon/intron boundary; cytochrome P-450; cancer;
KW abnormal drug response; environmental carcinogen; genotype; polymorphism;
KW drug candidate; protein malfunction; inhibitor; hypersensitivity; ss;
KW hyposensitivity.
XX
OS Homo sapiens.
XX
PN WO200120025-A2.
XX
PD 22-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-EP08570.
XX
PR 10-SEP-1999; 99EP-0118120.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Eiselt R;
XX
DR WPI; 2001-244818/25.
XX
PT Novel variant of CYP3A4 and CYP3A7 genes, associated with insufficient
PT metabolisation and/or sensitivity to drugs, useful for diagnosing and
PT treating diseases with drugs that are modulators of their gene product
PT -
XX
PS Claim 37; Fig 6; 106pp; English.
XX
CC The sequence represents a genomic sequence of exon 11 of the cytochrome
CC P-450 (CYP)3A4 gene. Polymorphic polynucleotides of the CYP3A4 or CYP3A7
CC genes are associated with abnormal drug response or individual
CC predisposition to several common cancers caused by environmental
CC carcinogens. Primer sequences can be used in the production of variant
CC CYP3A4 and CYP3A7 proteins in order to study the malfunction of the
CC proteins, and in diagnostic tests designed for the specific detection and
CC genotyping of CYP3A4 and CYP3A7 alleles in humans. The invention provides
CC methods for identifying and obtaining drug candidates and inhibitors of
CC the genes for therapy of disorders related to acquired drug hypo- or
CC hypersensitivity.
XX
SQ Sequence 11 BP; 3 A; 5 C; 1 G; 2 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCAGGGAG 11
|||||||||
Db 10 TTCAGGGAG 2

RESULT 16
AAS01933
ID AAS01933 standard; DNA; 11 BP.
XX
AC AAS01933;
XX
DT 04-JUL-2001 (first entry)
XX
DE Cytochrome P-450 (CYP)3A4 gene exon 11 antisense strand DNA #4.
XX
KW CYP3A4; CYP3A7; human; exon/intron boundary; cytochrome P-450; cancer;
KW abnormal drug response; environmental carcinogen; genotype; polymorphism;
KW drug candidate; protein malfunction; inhibitor; hypersensitivity; ss;
KW hyposensitivity.
XX
OS Homo sapiens.
XX
PN WO200120025-A2.
XX
PD 22-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-EP08570.
XX
PR 10-SEP-1999; 99EP-0118120.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Eiselt R;
XX
DR WPI; 2001-244818/25.
XX
PT Novel variant of CYP3A4 and CYP3A7 genes, associated with insufficient
PT metabolisation and/or sensitivity to drugs, useful for diagnosing and
PT treating diseases with drugs that are modulators of their gene product
PT -
XX
PS Claim 37; Page 45; 106pp; English.
XX
CC The sequence represents a genomic sequence of exon 11 of the cytochrome
CC P-450 (CYP)3A4 gene. Polymorphic polynucleotides of the CYP3A4 or CYP3A7
CC genes are associated with abnormal drug response or individual
CC predisposition to several common cancers caused by environmental
CC carcinogens. Primer sequences can be used in the production of variant
CC CYP3A4 and CYP3A7 proteins in order to study the malfunction of the
CC proteins, and in diagnostic tests designed for the specific detection and
CC genotyping of CYP3A4 and CYP3A7 alleles in humans. The invention provides
CC methods for identifying and obtaining drug candidates and inhibitors of
CC the genes for therapy of disorders related to acquired drug hypo- or
CC hypersensitivity.
XX
SQ Sequence 11 BP; 2 A; 1 C; 5 G; 3 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCAGGGAG 11
|||||||||
Db 2 TTCAGGGAG 10

RESULT 17
ABV63286/c
ID ABV63286 standard; cDNA; 11 BP.
XX
AC ABV63286;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1072.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX

PS Disclosure; Page 54; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCAGGGAG 11
|||||||||
Db 9 TTCAGGGAG 1

RESULT 18
ABV70707/c
ID ABV70707 standard; cDNA; 11 BP.
XX
AC ABV70707;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8493.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer -
XX
PS Claim 24; Page 271; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention.
XX
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCAGGGAG 11
|||||||||
Db 9 TTCAGGGAG 1

RESULT 19
ABQ86448/c
ID ABQ86448 standard; cDNA; 11 BP.
XX
AC ABQ86448;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 203.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15178.
XX
PR 03-JAN-2001; 2001DE-1000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and ageing, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential
PT gene expression -
XX
PS Claim 8; Page 45; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCAGGGAG 11
|||||||||
Db 9 TTCAGGGAG 1

RESULT 20
ABK72572
ID ABK72572 standard; DNA; 12 BP.

XX
AC ABK72572;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human OPA1 gene, exon/intron junction #39.
XX
KW Human; ophthalmological; OPA1; autosomal dominant optic atrophy;
KW ADOA; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200227022-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-GB04284.
XX
PR 26-SEP-2000; 2000GB-0023555.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (UYEY-) UNIV EYE HOSPITAL.
XX
PI Bhattacharya S, Wissinger B, Alexander C, Votruba M;
XX
DR WPI; 2002-416484/44.
XX
PT Novel human normal or mutant OPA1 (the predominant locus for autosomal
PT dominant optic atrophy (ADOA)) polypeptides and the OPA1 gene, useful
PT in the diagnosis and treatment of autosomal dominant optic atrophy ADOA
PT -
XX
PS Disclosure; Figure 12; 75pp; English.
XX
CC The invention relates to an isolated human normal or mutant OPA1 (the
CC predominant locus for autosomal dominant optic atrophy (ADOA))
CC polypeptide (I), characterised by a molecular weight of about 112 kDa,
CC and substantially free of other human proteins. Also described is the DNA
CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
CC treatment of a medical condition resulting from a defect in the OPA1
CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
CC and antibodies to (I) are useful in a variety of hybridisation and
CC immunological assays to screen for, and to detect the presence of, either
CC a normal or a defective OPA1 gene or gene product. ABK72533-ABK72593
CC represent the human OPA1 gene and intron/exon splice junctions.
XX
SQ Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 other;

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 TTCAGGGAG 11
              |||||||||
Db          2 TTCAGGGAG 10
```

RESULT 21
AAA56517
ID AAA56517 standard; DNA; 10 BP.
XX
AC AAA56517;
XX
DT 07-SEP-2000 (first entry)
XX
DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:411.
XX
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW disease onset mechanism; genetic disease; drug development; ss.
XX
OS Homo sapiens.
XX
PN WO200024892-A1.
XX
PD 04-MAY-2000.
XX
PF 28-OCT-1999; 99WO-JP05982.
XX
PR 28-OCT-1998; 98JP-0307532.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-350734/30.
XX
PT Genes most frequently expressed in human monocytes and GM-macrophages
PT and M-macrophages studied and with cDNAs characterized, for study of
PT gene specificity, disease onset mechanism, drug development and
PT diagnosis -
XX
PS Claim 37; Page 121; 138pp; Japanese.
XX
CC The present invention describes 100 human genes, which are expressed
CC most frequently in human monocytes. The cDNA of each gene has a
CC sequence fully defined in the specification, and lacking the CATG
CC sequence located adjacent to polyA region. Also described are:
CC (1) an antibody specifically for the protein encoded by any of the
CC genes; (2) oligonucleotides obtained from the cDNA sequences;
CC (3) 380 human genes which are expressed most frequently in human
CC macrophages, differentiated from human monocytes by
CC granulocyte-macrophage colony-stimulating factor, the cDNA of each gene
CC has a fully defined sequence, given in the specification, lacking the
CC base sequence CATG located most closely to the poly A region;
CC (4) an antibody specifically for the protein encoded by any of the
CC genes of (3); and (5) oligonucleotides obtained from the cDNA sequences
CC of (3). The genes and cDNAs, are used for the study of gene specificity
CC and disease onset mechanism e.g. oncogenesis, genetic diseases, drug
CC development and diagnosis. AAA56107 to AAA56586 represent specifically
CC claimed oligonucleotide tag sequences for human genes expressed in
CC monocytes and macrophages.
XX
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          9 GAGCCCGTGC 18
              | ||||||||
Db          1 GTGCCCGTGC 10
```

RESULT 22
AAA14247
ID AAA14247 standard; DNA; 10 BP.
XX
AC AAA14247;
XX
DT 21-JUL-2000 (first entry)
XX
DE Camel male-associated sequence PCR primer OPAN.06.
XX
KW Camel; dromedary; male-specific; chromosome Y; sex determination;
KW PCR primer; ss.
XX
OS Camelus dromedarius.
XX
PN WO200017347-A1.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-AU00821.
XX

PR 23-SEP-1998; 98AU-0006108.
XX
PA (CAME-) CAMELOT BIOSCIENCE.
PA (KING/) KING M E.
XX
PI Harrison BT, King BW, Mitchell RW, Reed KC, Wade NM, King ME;
XX
DR WPI; 2000-386934/33.
XX
PT New polynucleotide useful for determining sex of camelids, hybridizes
PT specifically to camelid Y chromosome -
XX
PS Example 1; Page 17; 69pp; English.
XX
CC The invention relates to novel male-specific nucleotide sequences from
CC camelids, and to methods of determining the sex of a camelid, a
CC camelid foetus or embryo, or camelid cells. Sequences AAA14222 and
CC AAA14238- AAA14243, which are located on the Y chromosome of the
CC dromedary (Camelus dromedarius) are claimed. These sequences, or their
CC homologues from other camelids form the basis of the sex determination
CC method of the invention. A camelid male-specific sequence (particularly
CC CY.AM11; AAA14222) is amplified by PCR and then detected via
CC hybridisation. Amplification of CY.AM11 (or other male-specific fragment
CC is performed simultaneously with the amplification of a control autosomal
CC fragment (CA.AN06; AAA14225). The presence of both CY.AM11 and CA.AN06
CC indicate that the sample is from a male; the presence of CA.AN06 only
CC indicates that the sample is from a female. The male-specific sequences,
CC and probes and primers derived therefrom, are used for sex determination
CC of of camelids, particularly dromedaries, and to determine the sex
CC chromosome constitution of a sperm cell from a camelid. The sequences may
CC also be used to screen recombinant DNA libraries from different mammalian
CC species, to deduce similar sequences of genetically linked sequences
CC having similar functionality, and in chromosome walking or jumping
CC techniques. The new sequences are associated uniquely with the camelid Y
CC chromosome and sex analysis may be performed where only a small number of
CC cells is available from a microscopic biopsy. Sequences AAA14245-A14249
CC represent PCR primers used in an exemplification of the inevntion to
CC isolate male-associated DNA fragments from camel genomic DNA. One of
CC these male-associated fragments was CY.AM11.
XX
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GGGAGCCCGT 16
|||| ||||| |
Db 1 GGGAACCCGT 10

RESULT 23
AAZ78376/c
ID AAZ78376 standard; DNA; 10 BP.
XX
AC AAZ78376;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:804.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13800.
XX
PR 19-JUN-1998; 98US-0089833.
PR 19-JUN-1998; 98US-0089844.
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089878.
PR 19-JUN-1998; 98US-0089991.
PR 19-JUN-1998; 98US-0089992.
PR 19-JUN-1998; 98US-0089993.
PR 19-JUN-1998; 98US-0089994.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0089999.
PR 19-JUN-1998; 98US-0090000.
PR 19-JUN-1998; 98US-0090035.
PR 19-JUN-1998; 98US-0090036.
PR 19-JUN-1998; 98US-0090039.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PR 19-JUN-1998; 98US-0090042.
PR 19-JUN-1998; 98US-0090043.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090045.
PR 19-JUN-1998; 98US-0090047.
PR 19-JUN-1998; 98US-0090048.
PR 19-JUN-1998; 98US-0090072.
PR 19-JUN-1998; 98US-0090076.
PR 19-JUN-1998; 98US-0090077.
PR 19-JUN-1998; 98US-0090078.
PR 19-JUN-1998; 98US-0090079.
PR 19-JUN-1998; 98US-0090080.
PR 08-DEC-1998; 98US-0111715.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer -
XX
PS Claim 1; Page 88; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or
CC ESTs (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can
CC lyse the tumour cells, immunostimulatory cofactors also being required
CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell
CC differentially expressed genes, or of their encoded proteins, can be used
CC to identify cells as belonging to the monocyte lineage. Cells containing
CC these genes can be used in active immunotherapy (or to stimulate
CC production of a population of antigen-specific effector cells) and
CC vectors containing them are used in gene therapy. Co-administration of
CC tumour antigens and APC-associated costimulatory factors ensures adequate
CC antigen presentation to endogenous APCs and upregulates the APCs for the

```
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              ||| ||||||
Db         10 TCAAGGAGCC 1


RESULT 24
AAZ81654/c
ID   AAZ81654 standard; DNA; 10 BP.
XX
AC   AAZ81654;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #888.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 82; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              ||| ||||||
Db         10 TCAAGGAGCC 1


RESULT 25
AAZ82050
ID   AAZ82050 standard; DNA; 10 BP.
XX
AC   AAZ82050;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1284.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 93; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
```

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CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 GAGCCCGTGC 18
              | ||||||||
Db          1 GTGCCCGTGC 10


RESULT 26
AAZ83201
ID   AAZ83201 standard; DNA; 10 BP.
XX
AC   AAZ83201;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2435.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 124; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGGA 10
              || |||||||
Db          1 GCCTCAGGGA 10


RESULT 27
AAZ84054
ID   AAZ84054 standard; DNA; 10 BP.
XX
AC   AAZ84054;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3288.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 147; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
```

```
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GCCCGTGCGG 20
               |||||| |||
Db          1 GCCCGTCCGG 10


RESULT 28
AAZ84542/c
ID   AAZ84542 standard; DNA; 10 BP.
XX
AC   AAZ84542;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3776.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 159; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGGA 10
                |||| |||||
Db         10 GCTTAAGGGA 1


RESULT 29
AAZ85030
ID   AAZ85030 standard; DNA; 10 BP.
XX
AC   AAZ85030;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4264.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 172; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
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CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              ||||||||  |
Db          1 GGGAGCCCCT 10


RESULT 30
AAZ85257
ID   AAZ85257 standard; DNA; 10 BP.
XX
AC   AAZ85257;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4491.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 179; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 5 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              ||||||||  |
Db          1 CAGGGAGCGC 10


RESULT 31
AAZ85646
ID   AAZ85646 standard; DNA; 10 BP.
XX
AC   AAZ85646;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4880.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 189; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
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CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              | ||||||||
Db          1 CTGGGAGCCC 10


RESULT 32
AAZ85771/c
ID   AAZ85771 standard; DNA; 10 BP.
XX
AC   AAZ85771;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5005.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 192; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGGA 10
              |||| |||||
Db         10 GCTTTAGGGA 1


RESULT 33
AAH63939
ID   AAH63939 standard; cDNA; 10 BP.
XX
AC   AAH63939;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 779.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 57; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
```

```
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              ||||||||| |
Db          1 GGGAGCCCCT 10


RESULT 34
AAH63940
ID   AAH63940 standard; cDNA; 10 BP.
XX
AC   AAH63940;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 780.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 57; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              ||||||||| |
Db          1 GGGAGCCCCT 10


RESULT 35
AAH20558
ID   AAH20558 standard; DNA; 10 BP.
XX
AC   AAH20558;
XX
DT   09-AUG-2001  (first entry)
XX
DE   Human MTR1 exon14/intron14 junction.
XX
KW   MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW   transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW   11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW   intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW   cell growth; cell death; cell differentiation; urogenital disease;
KW   polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW   rhabdomyosarcoma; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..5
FT                   /*tag=  a
FT                   /number= 14
FT   intron          6..10
FT                   /*tag=  b
FT                   /number= 14
XX
PN   WO200132693-A2.
XX
PD   10-MAY-2001.
XX
PF   06-NOV-2000; 2000WO-DE03876.
XX
PR   04-NOV-1999;   99DE-1053167.
XX
PA   (UYGU-) UNIV GUTENBERG JOHANNES.
XX
PI   Prawitt D;  Pelletier J,  Zabel B;
XX
DR   WPI; 2001-316417/33.
XX
PT   DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
PT   syndrome and tumors, also related proteins and antibodies -
XX
PS   Example 2; Fig 2; 46pp; German.
XX
CC   This invention describes a novel DNA sequence (I) encoding the MTR1
CC   protein that: (i) has at least one biological activity of a TRP
CC   (transient receptor potential) family protein; (ii) is connected with
CC   etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC   with tumors involving 11p15.5 abnormalities. The products of the
CC   invention have anticancer and developmental activity. MRT1 is involved in
CC   regulation of intracellular calcium ion levels, which are essential for
CC   cellular responses to hormones and/or growth factors; also in apoptosis
CC   and cell growth, death and differentiation, and in urogenital diseases,
CC   including polycystic kidney disease. (I) and related ribozymes, antisense
CC   RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases
CC   associated with altered expression of the MRT1 gene or activity of its
CC   protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC   rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC   used for diagnosis of such diseases. (I) can also be used for recombinant
CC   production of MRT1 proteins (II) (used for analysis, characterization and
CC   therapy), as tissue or chromosomal markers, for identifying genetic
CC   diseases and related sequences, as primers for genetic fingerprinting, as
CC   source of oligonucleotides for biochips, and to raise anti-protein or
CC   anti-DNA antibodies. (II) are used to raise Ab, as reagents in
CC   competitive assays for (II), as tissue markers; for identifying
CC   interacting proteins and in screening for (ant)agonists. This sequence
CC   represents human MTR1 gene exon 14/intron 14 junction region described in
CC   the method of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
```

```
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGCCCGTGCG 19
              |||| |||||
Db          1 AGCCGGTGCG 10


RESULT 36
AAH32842
ID   AAH32842 standard; cDNA; 10 BP.
XX
AC   AAH32842;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:215.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001069993-A.
XX
PD   21-MAR-2001.
XX
PF   28-APR-2000; 2000JP-0131079.
XX
PR   08-JUL-1999;   99JP-0195103.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-304369/32.
XX
PT   LPS activated human monocyte expression gene group  -
XX
PS   Claim 19; Page 38; 52pp; Japanese.
XX
CC   The present invention describes an lipopolysaccharide (LPS) activated
CC   human monocyte expression gene group consisting of the high-ranking 50
CC   genes of the highest expression among the genes expressed by human
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
CC   development of new means for the diagnosis and the treatment of various
CC   human diseases in which human monocyte plays an important role.
CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
CC   monocyte expression gene cDNA tags from the present invention. AAH32944
CC   represents an LPS activated human monocyte expression gene cDNA sequence
CC   encoding AAB98009, which are given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 GAGCCCGTGC 18
              | ||||||||
Db          1 GTGCCCGTGC 10


RESULT 37
AAF75023
ID   AAF75023 standard; DNA; 10 BP.
XX
AC   AAF75023;
XX
DT   08-MAY-2001  (first entry)
XX
DE   HTR1A gene polymorphism primer #13.
XX
KW   5-hydroxy tryptamine receptor 1A; HTR1A; polymorphism; Tourette's;
KW   neuropsychiatric; ss.
XX
OS   Homo sapiens.
XX
PN   WO200110884-A1.
XX
PD   15-FEB-2001.
XX
PF   01-AUG-2000; 2000WO-US40519.
XX
PR   06-AUG-1999;   99US-0147711.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Denton RR,  Kliem SE,  Nandabalan K,  Stephens JC;
XX
DR   WPI; 2001-191514/19.
XX
PT   New 5-hydroxy tryptamine receptor 1A gene variants for studying
PT   expression and biological function of the gene and for developing drugs
PT   targeting 5-hydroxy tryptamine receptor 1A protein  -
XX
PS   Disclosure; Page 22; 64pp; English.
XX
CC   The present invention relates to 5-hydroxy tryptamine receptor 1A
CC   (HTR1A) gene. HTR1A-encoding polynucleotides containing one or more
CC   of the novel polymorphic sites are useful in studying the
CC   expression and biological function of HTR1A, as well as
CC   in developing drugs targeting this protein. In addition,
CC   information on the combinations of polymorphisms
CC   in the HTR1A gene may have diagnostic and forensic applications.
CC   A polymorphic variant of HTR1A is useful in studying the
CC   effect of the variation on the biological activity of HTR1A
CC   as well as studying the binding affinity of candidate drugs
CC   targeting HTR1A for the treatment of neuropsychiatric diseases
CC   and Tourette's syndrome.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 5 G; 0 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              |||||||| |
Db          1 CAGGGAGCGC 10


RESULT 38
AAF40219/c
ID   AAF40219 standard; DNA; 10 BP.
XX
AC   AAF40219;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6958.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US16223.
XX
PR   16-JUN-1999;   99US-0335032.
```

XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 248; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 GGGAGCCCGT 16
              ||||||||| |
Db         10 GGGAGCCCAT 1
```

RESULT 39
AAF42414
ID AAF42414 standard; DNA; 10 BP.
XX
AC AAF42414;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9153.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 326; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         11 GCCCGTGCGG 20
                ||| ||||||
Db          1 GCCGGTGCGG 10
```

RESULT 40
AAL48143/c
ID AAL48143 standard; DNA; 10 BP.
XX
AC AAL48143;
XX
DT 27-SEP-2002 (first entry)
XX
DE Human neuropeptide Y primer extension oligo SEQ ID NO: 67.
XX
KW Human; neuropeptide Y; NPY; isogene; SNP; atherosclerosis; obesity;
KW psychological disorder; single nucleotide polymorphism; alcoholism;
KW antiarteriosclerotic; anorectic; PCR; primer extension oligonucleotide;
KW ss.
XX
OS Homo sapiens.

XX
PN WO200251857-A1.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2000; 2000WO-US34758.
XX
PR 21-DEC-2000; 2000WO-US34758.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Lanz EM, Nandabalan K, Stephens JC;
XX
DR WPI; 2002-566671/60.
XX
PT New genetic variants of the human Neuropeptide Y (NPY) gene useful for
PT treating disorders affected by abnormal expression or function of NPY
PT isogene e.g., atherosclerosis or obesity -
XX
PS Disclosure; Page 17; 80pp; English.
XX
CC The present invention provides the human neuropeptide Y (NPY) gene and
CC single nucleotide polymorphisms (SNPs) identified therein. The sequence
CC can be used in the treatment of disorders associated with NPY, including
CC atherosclerosis, obesity, psychological disorders and alcoholism. The
CC present sequence is an allele specific primer extension oligonucleotide
CC used to isolate the human NPY coding sequence.
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         10 AGCCCGTGCG 19
               ||||||| ||
Db         10 AGCCCGTCCG 1
```

RESULT 41
ABK81799
ID ABK81799 standard; DNA; 10 BP.
XX
AC ABK81799;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human CHRM5 gene polymorphism detection oligonucleotide primer #5.
XX
KW Human; cholinergic receptor muscarinic 5; CHRM5; genotyping; haplotyping;
KW single nucleotide polymorphism; SNP; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200232924-A2.
XX
PD 25-APR-2002.
XX
PF 11-OCT-2001; 2001WO-US32022.
XX
PR 19-OCT-2000; 2000WO-US29071.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Chew A, Choi JY, Denton RR, Nandabalan K;
PI Sausker EA, Stephens JC;
XX
DR WPI; 2002-435523/46.
XX
PT Novel cholinergic receptor, muscarinic 5 polynucleotide useful
PT therapeutically and in screening for candidate drug to treat diseases
PT related to the receptor activity -
XX
PS Claim 16; Page 14; 72pp; English.
XX
CC The present invention relates to a new cholinergic receptor, muscarinic 5
CC (CHRM5) polynucleotide comprising a sequence which is a polymorphic
CC variant for a reference sequence for the CHRM5 gene or its fragment,
CC or a polymorphic variant of a reference sequence for a CHRM5 cDNA or
CC its fragment. The invention is useful in drug screening assays. The
CC molecules of the invention are useful in studying the expression and
CC function of CHRM5, and in expressing CHRM5 protein for use in screening
CC for candidate drugs to treat diseases related to CHRM5 activity. The
CC methods of the invention are useful in developing diagnostic tests and
CC therapeutic treatments. The method is also useful in the design of
CC clinical trials of candidate drugs for treating specific condition or
CC disease associated with CHRM5 activity and is useful in determining
CC whether an individual has one of the haplotypes or one of the haplotype
CC pairs. The invention is useful in a variety of diagnostic and prognostic
CC formats and therapeutic methods. The invention is also useful in
CC genotyping and/or haplotyping the CHRM5 gene in an individual. The
CC present nucleic acid sequence represents one of a collection of
CC oligonucleotide primers (ABK81795-ABK81814) that were used in the
CC invention to detect polymorphisms in the human CHRM5 gene.
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 GGGAGCCCGT 16
              ||||||| ||
Db          1 GGGAGCCTGT 10
```

RESULT 42
AAS98841
ID AAS98841 standard; DNA; 10 BP.
XX
AC AAS98841;
XX
DT 26-MAR-2002 (first entry)
XX
DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #207.
XX
KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW cytostatic; gene therapy; malignant histiocytosis; isogene;
KW myeloid malignancy; inflammatory disorder; transgenic animal;
KW haplotype; genotype; human; allele specific oligonucleotide; ASO;
KW primer; primer extension; ss.
XX
OS Homo sapiens.
XX
PN WO200179225-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US12044.
XX
PR 12-APR-2000; 2000US-196411P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075058/10.
XX
PT Novel polymorphic variants of colony stimulating factor 1 receptor
PT useful in studying expression and function of the protein, useful for
PT screening candidate drugs to treat diseases e.g. inflammatory disorders
PT -
XX
PS Claim 17; Page 17; 164pp; English.
XX
CC The invention describes a novel isolated polynucleotide (I) comprising a

CC sequence which is a polymorphic variant (PV) of a reference sequence for
CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
CC polypeptide are useful for improving the discovery and development of
CC drugs for treating diseases associated with CSF1R activity, e.g.,
CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
CC and the haplotypes can be used to validate CSF1R as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
CC be used in developing diagnostic tests and therapeutic treatments. (I) is
CC useful in studying the expression and function of CSF1R, and in
CC expressing CSF1R protein for use in screening for candidate drugs to
CC treat diseases related to CSF1R activity and in studying the effect of
CC the variation on the biological activity of CSF1R as well as on the
CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
CC useful in a variety of diagnostic and prognostic formats and therapeutic
CC methods. A transgenic animal is useful in studying expression of the
CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against CSF1R protein, and for testing the efficacy of
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC are useful as probes and primers, and for assaying a polymorphism in the
CC target region. Without requiring any a priori knowledge of the phenotypic
CC effect of any particular CSF1R or haplotype the invention provides a
CC method for identifying lead compounds that are more likely to show
CC efficacy in clinical trials. This sequence is a primer used to detect
CC CSF1R gene polymorphisms by primer extension, described in the method of
CC the invention.
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 AGGGAGCCCG 15
              |||||||| |
Db          1 AGGGAGCCTG 10
```

RESULT 43
AAD25027
ID AAD25027 standard; DNA; 10 BP.
XX
AC AAD25027;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human AANAT gene polymorphism detecting primer #17.
XX
KW Human; genetic variant; arylalkylamine N-acetyltransferase; AANAT gene;
KW haplotyping; genotyping; pineal gland disorder; melatonin synthesis;
KW gene therapy; antisense therapy; primer; polymorphism; ss.
XX
OS Homo sapiens.
XX
PN WO200187909-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16279.
XX
PR 18-MAY-2000; 2000US-205068P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kazemi A, Nandabalan K;
XX
DR WPI; 2002-055682/07.
XX
PT New genetic variants of human arylalkylamine N-acetyltransferase
PT (AANAT) gene for studying expression, function of the gene and
PT expressing AANAT protein for use in screening for drugs to treat
PT disorders of pineal gland -
XX
PS Claim 18; Page 13; 67pp; English.
XX
CC The patent discloses novel genetic variants of the arylalkylamine
CC N-acetyltransferase (AANAT) gene. The invention also relates to
CC compositions and methods for haplotyping and/or genotyping the
CC AANAT gene. Polymorphic variants of AANAT protein are useful for
CC screening for drugs targeting the polypeptide. AANAT polynucleotides
CC are useful for studying the expression and function of AANAT and for
CC expressing AANAT protein for use in screening for candidate drugs to
CC treat diseases related to AANAT activity. The methods are used to
CC develop diagnostic tests and therapeutic treatment for disorders of
CC pineal gland that derive from defects in melatonin synthesis. It is
CC useful for determining whether an individual has one of the haplotypes
CC 1-4 or the haplotype pairs. The haplotyping method is useful to validate
CC AANAT as a candidate target for treating a specific condition or disease
CC predicted to be associated with AANAT activity. AANAT sequences of the
CC invention are also used in gene therapy and antisense therapy. The
CC present DNA sequence is a primer which is used for detecting human
CC AANAT gene polymorphisms.
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 U; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              ||||||| ||
Db          1 CAGGGAGGCC 10
```

RESULT 44
ABL42775
ID ABL42775 standard; cDNA; 10 BP.
XX
AC ABL42775;
XX
DT 12-APR-2002 (first entry)
XX
DE Human maturation/activation dendritic cell expression gene tag #149.
XX
KW Human; maturation/activation dendritic cell expression gene; tag;
KW maturation; activation; dendritic cell; ss.
XX
OS Homo sapiens.
XX
PN JP2001327293-A.
XX
PD 27-NOV-2001.
XX
PF 22-MAY-2000; 2000JP-0150562.
XX
PR 22-MAY-2000; 2000JP-0150562.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-127070/17.
XX
PT Human maturation/activation dendritic cell expression gene group -
XX
PS Claim 10; Page 13; 41pp; Japanese.
XX
CC The present invention describes a human maturation/activation dendritic
CC cell (DC) expression gene group consisting of 100 genes which show the
CC highest expression among the genes expressed in human maturation/
CC activation DC. Also described are: (1) a protein expressed by the above
CC human maturation/activation DC expression gene; (2) an antibody against
CC the protein; and (3) an antagonist against the expression of each gene
CC belonging to the above gene group. The gene group is useful for the
CC treatment and the diagnosis of various human diseases related to human
CC DC. ABL42627 to ABL42926 represent specifically claimed human
CC maturation/activation DC expression gene tags from the present invention.
XX

```
SQ   Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 GAGCCCGTGC 18
              | ||||||||
Db          1 GTGCCCGTGC 10


RESULT 45
ABT14329
ID   ABT14329 standard; DNA; 10 BP.
XX
AC   ABT14329;
XX
DT   20-FEB-2003  (first entry)
XX
DE   Nucleic acid PCR amplification method-related RAPD PCR primer #99.
XX
KW   Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW   RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS   Unidentified.
XX
PN   WO200281743-A2.
XX
PD   17-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-GB01489.
XX
PR   02-APR-2001; 2001GB-0008182.
XX
PA   (HAMI/) HAMILL B.
XX
PI   Hamill B;
XX
DR   WPI; 2003-075484/07.
XX
PT   Amplification of nucleotide sequences from polynucleotides by chain
PT   extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT   solution, 2 attached to supports and both share complementary sequences
PT   .
XX
PS   Disclosure; Fig 17; 60pp; English.
XX
CC   The invention comprises a method for the PCR amplification of nucleic
CC   acids. The method involves a set of primers, where two of the primers are
CC   in solution and at least two other primers are attached to a solid
CC   support. The method of the invention can be used for the analysis of a
CC   nucleic acid or a mixture of nucleic acids, including: single-stranded
CC   DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC   present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC   PCR primer of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCCGT 16
              |||| |||||
Db          1 GGGAACCCGT 10


RESULT 46
AAQ51997/c
ID   AAQ51997 standard; RNA; 11 BP.
XX
AC   AAQ51997;
XX
DT   25-MAR-2003  (updated)
DT   26-MAY-1994  (first entry)
XX
DE   B-cell mRNA ribozyme cleavable nucleotide 1272.
XX
KW   Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW   resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW   actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW   adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW   human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW   B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW   neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW   hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
OS   Homo sapiens.
XX
PN   WO9323057-A1.
XX
PD   25-NOV-1993.
XX
PF   13-MAY-1993;   93WO-US04573.
XX
PR   14-MAY-1992;   92US-0882822.
PR   14-MAY-1992;   92US-0882885.
PR   26-AUG-1992;   92US-0936110.
PR   26-AUG-1992;   92US-0936421.
PR   26-AUG-1992;   92US-0936422.
PR   26-AUG-1992;   92US-0936531.
PR   26-AUG-1992;   92US-0936532.
PR   07-DEC-1992;   92US-0987131.
PR   19-JAN-1993;   93US-0006122.
PR   19-JAN-1993;   93US-0008910.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Draper KG,  Thompson JD;
XX
DR   WPI; 1993-386203/48.
XX
PT   New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT   associated with tumours or mRNA expressed from gene encoding
PT   multiple drug resistance
XX
PS   Claim 3; Fig 7; 69pp; English.
XX
CC   The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC   associated with development or maintenance of chronic myelogenous
CC   leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC   acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC   lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC   and lung cancer.  The full length mRNAs containing these target
CC   sequences, encode aberant cellular proteins which are able to control
CC   cellular proliferation and are directly linked to a leukemic
CC   phenotype.  These target sequences are identified by the ribozyme of
CC   the invention.  The ribozymes is formed in a hammerhead motif, but may
CC   also be formed in the motif of a hairpin, hepatitis delta virus, group
CC   I intron or RNaseP-like RNA.  These ribozymes may be used to inhibit
CC   the development or expression of a transformed phenotype in man and
CC   other animals by modulating expression of the corresponding gene.
CC   Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC   cells elicits inhibition of the transformed state.  Multiple drug
CC   resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC   drug resistance used by transformed cells and thus enhances drug
CC   therapies for tumours.  The ribozymes may also be used to study
CC   genetic drift and mutations within cells.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 11 BP; 1 A; 6 C; 2 G; 2 U; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          8 GGAGCCCGTG 17
              ||||| ||||
Db         11 GGAGCACGTG 2
```

RESULT 47
AAS02884
ID AAS02884 standard; DNA; 11 BP.
XX
AC AAS02884;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human pregnane X receptor (hPXR) gene, PCR primer #154.
XX
KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
KW therapeutic; chemotherapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200120026-A2.
XX
PD 22-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-EP08827.
XX
PR 10-SEP-1999; 99EP-0118120.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Hustert E;
XX
DR WPI; 2001-273428/28.
XX
PT Novel variant of the human pregnane X receptor gene, associated with
PT insufficient metabolisation and/or sensitivity to drugs, is useful for
PT diagnosing and treating diseases with drugs that are modulators of
PT their gene product -
XX
PS Claim 37; Page 46; 108pp; English.
XX
CC AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding
CC sequences and PCR primers of the invention. The human pregnane X
CC receptor sequences are used to make antibodies, or a substance capable of
CC binding specifically to the gene product of hPXR gene, for diagnosing and
CC treating various diseases, such as cancer, with drugs that are
CC substrates, inhibitors or modulators of the hPXR gene product. The
CC proteins can be used to identify and obtain prodrugs and drugs for
CC treatment of diseases which are amenable to chemotherapy. The nucleic
CC acids can be used in gene therapy for the treatment or prevention of
CC disorders associated with hPXR expression.
XX
SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 TCAGGGAGCC 13
              | ||||||||
Db          2 TGAGGGAGCC 11
```

RESULT 48
AAS02885/c
ID AAS02885 standard; DNA; 11 BP.
XX
AC AAS02885;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human pregnane X receptor (hPXR) gene, PCR primer #155.
XX
KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
KW therapeutic; chemotherapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200120026-A2.
XX
PD 22-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-EP08827.
XX
PR 10-SEP-1999; 99EP-0118120.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Hustert E;
XX
DR WPI; 2001-273428/28.
XX
PT Novel variant of the human pregnane X receptor gene, associated with
PT insufficient metabolisation and/or sensitivity to drugs, is useful for
PT diagnosing and treating diseases with drugs that are modulators of
PT their gene product -
XX
PS Claim 37; Page 46; 108pp; English.
XX
CC AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding
CC sequences and PCR primers of the invention. The human pregnane X
CC receptor sequences are used to make antibodies, or a substance capable of
CC binding specifically to the gene product of hPXR gene, for diagnosing and
CC treating various diseases, such as cancer, with drugs that are
CC substrates, inhibitors or modulators of the hPXR gene product. The
CC proteins can be used to identify and obtain prodrugs and drugs for
CC treatment of diseases which are amenable to chemotherapy. The nucleic
CC acids can be used in gene therapy for the treatment or prevention of
CC disorders associated with hPXR expression.
XX
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 TCAGGGAGCC 13
              | ||||||||
Db         10 TGAGGGAGCC 1
```

RESULT 49
ABV66076/c
ID ABV66076 standard; cDNA; 11 BP.
XX
AC ABV66076;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3862.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP15179.
XX
PR 03-JAN-2001; 2001DE-1000127.
XX
PA (HENK) HENKEL KGAA.

```
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 132; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGGAG 11
              | ||||||||
Db         11 CATCAGGGAG 2


RESULT 50
ABV66183/c
ID   ABV66183 standard; cDNA; 11 BP.
XX
AC   ABV66183;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3969.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 135; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 0 A; 5 C; 5 G; 1 T; 0 other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              ||||| ||||
Db         10 CAGGGGGCCC 1


RESULT 51
ABV66944
ID   ABV66944 standard; cDNA; 11 BP.
XX
AC   ABV66944;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4730.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 155; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 2 A; 4 C; 5 G; 0 U; 0 other;
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              ||||||| |
Db          1 CAGGGAGCGC 10
```

```
RESULT 52
ABV67117/c
ID   ABV67117 standard; cDNA; 11 BP.
XX
AC   ABV67117;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4903.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 160; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 other;
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GGAGCCCGTG 17
              ||||| ||||
Db         11 GGAGCGCGTG 2
```

```
RESULT 53
ABV68697/c
ID   ABV68697 standard; cDNA; 11 BP.
XX
AC   ABV68697;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6483.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP15179.
XX
PR   03-JAN-2001; 2001DE-1000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer  -
XX
PS   Disclosure; Page 205; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention.
XX
SQ   Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 other;
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAGCC 13
              ||| ||||||
Db         10 TCAAGGAGCC 1
```

```
RESULT 54
ABQ87254/c
ID   ABQ87254 standard; cDNA; 11 BP.
XX
AC   ABQ87254;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 1009.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
```

XX
PF 20-DEC-2001; 2001WO-EP15178.
XX
PR 03-JAN-2001; 2001DE-1000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and ageing, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential
PT gene expression -
XX
PS Claim 8; Page 79; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention.
XX
SQ Sequence 11 BP; 0 A; 5 C; 5 G; 1 T; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              ||||| ||||
Db         10 CAGGGGGCCC 1
```

RESULT 55
ABL51577/c
ID ABL51577 standard; DNA; 11 BP.
XX
AC ABL51577;
XX
DT 03-JUL-2002 (first entry)
XX
DE Transferrin receptor gene related oligonucleotide fragment #7.
XX
KW Polymorphism; single nucleotide polymorphism; SNP; identification;
KW detection; hybridisation; genotyping; transferrin receptor; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200221098-A2.
XX
PD 14-MAR-2002.
XX
PF 04-SEP-2001; 2001WO-US27446.
XX
PR 05-SEP-2000; 2000US-0655104.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Stanton VP, Wolfe JL, Kawate T, Verdine GL;
XX
DR WPI; 2002-362259/39.
XX
PT Detecting polymorphism in a polynucleotide (N) comprises hybridizing an
PT oligonucleotide with a variant (N) having modified nucleotides
PT incorporated at each point of suspected polymorphism occurrence -
XX
PS Example 4; Fig 29b; 245pp; English.
XX
CC The present invention describes a method for detecting a polymorphism
CC (P) in polynucleotide (N). The method comprises: (1) hybridising
CC oligonucleotides with fragments of (N) segments which contain a
CC polymorphism, and have modified nucleotides that are incorporated at
CC each point of occurrence of suspected (P) during amplification; and
CC (2) analysing the hybridising fragments for an incorporated detectable
CC label identifying the susceptible polymorphism. The method is used for
CC detecting polymorphisms (e.g. a single nucleotide polymorphism (SNP), a
CC deletion or a insertion) in (N). The method is useful for developing
CC diagnostic and prognostic tools for detecting a predisposition of
CC certain disease and disorders. The method is useful for detecting
CC variance in DNA sequencing, and has applications in genotyping. The
CC present sequence represents a transferrin receptor gene related
CC oligonucleotide sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGCCC 14
              |||||||| |
Db         10 CAGGGAGCAC 1
```

RESULT 56
AAT09422/c
ID AAT09422 standard; DNA; 8 BP.
XX
AC AAT09422;
XX
DT 25-MAR-2003 (updated)
DT 21-JUN-1996 (first entry)
XX
DE 5'-primer used for characterisation of human biological samples.
XX
KW 5'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PT used for genome mapping and disease diagnosis
XX
PS Claim 5; Page 44; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer
CC kit with 1361 possible primer pairs. The kit is used in a new method
CC for the characterisation of nucleic acid sequences obtd. from human
CC biological samples, which comprises PCR amplification and indexing of

```
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 2 A; 3 C; 2 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGG 9
              ||||||||
Db          8 CTTCAGGG 1


RESULT 57
AAT09561
ID   AAT09561 standard; DNA; 8 BP.
XX
AC   AAT09561;
XX
DT   25-MAR-2003  (updated)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 1 A; 2 C; 3 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGG 9
              ||||||||
Db          1 CTTCAGGG 8


RESULT 58
AAZ65526/c
ID   AAZ65526 standard; DNA; 9 BP.
XX
AC   AAZ65526;
XX
DT   30-MAR-2000  (first entry)
XX
DE   Immunosuppressant inhibitor oligonucleotide TGF-beta1-98-14.
XX
KW   Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW   vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW   prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW   monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
KW   glomerulonephritis; acute respiratory distress syndrome; ss;
KW   atherosclerosis.
XX
OS   Unidentified.
XX
PN   WO9963975-A2.
XX
PD   16-DEC-1999.
XX
PF   10-JUN-1999;   99WO-EP04013.
XX
PR   10-JUN-1998;   98EP-0110709.
PR   25-JUL-1998;   98EP-0113974.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Schlingensiepen K,  Schlingensiepen R,  Brysch W;
XX
DR   WPI; 2000-097470/08.
XX
PT   Composition containing immune stimulant and inhibitor of agent that
PT   adversely affects the immune response, for treating cancers and
PT   infections -
XX
PS   Claim 10; Figure 1; 30pp; English.
XX
CC   This sequence is an immunosuppressant inhibitor oligonucleotide, which
CC   is used in the invention. The invention relates to a composition which
CC   contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC   transforming growth factor TGF-beta, vascular endothelial growth factor
CC   VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC   that adversely affects the immune response. The composition also includes
CC   at least one stimulant that positively affects the immune response. This
CC   oligonucleotide is an example of an inhibitor that is used in the
CC   composition. The composition is used as an immunostimulant for the
CC   treatment of neoplasms and infections, particularly hyperproliferation;
CC   leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC   colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC   breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC   malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC   most of which are directed against TGFbeta or VEGF, are inhibitors of
CC   monocyte chemotactic protein-1 (MCP-1) and are useful as
CC   anti-inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
CC   colitis, diabetes, glomerulonephritis, acute respiratory distress
CC   syndrome and the formation of atherosclerotic plaque.
XX
SQ   Sequence 9 BP; 0 A; 4 C; 4 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GGAGCCCG 15
              ||||||||
Db          8 GGAGCCCG 1
```

```
RESULT 59
AAX32621/c
ID   AAX32621 standard; DNA; 10 BP.
XX
AC   AAX32621;
XX
DT   23-JUN-1999  (first entry)
XX
DE   Anticancer duplex forming oligonucleotide SEQ ID #21.
XX
KW   Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW   multiple drug resistance; MDR; ss.
XX
OS   Synthetic.
XX
PN   WO9523162-A1.
XX
PD   31-AUG-1995.
XX
PF   27-FEB-1995;   95WO-US02419.
XX
PR   28-FEB-1994;   94US-0202927.
XX
PA   (MICR-) MICROPROBE CORP.
PA   (UYYA ) UNIV YALE.
XX
PI   Cheng Y,  Lukhtanov EA,  Meyer RB,  Pai BS,  Reed MW;
PI   Zhou JH;
XX
DR   WPI; 1995-311501/40.
XX
PT   New stable oligonucleotide duplex with 3'-steroid gp - including
PT   intramolecular duplex with hairpin loop region, having selective
PT   cytotoxicity against some tumour cells
XX
PS   Disclosure; Page 52; 107pp; English.
XX
CC   New oligonucleotides are disclosed which are 8-18 nucleotides in
CC   length and which have a steroid structure attached to the 3'-end
CC   through a linker attached to the A-ring of the steroid skeleton.
CC   In particular, the present sequence has a cholesterol moiety attached
CC   by its A-ring to to the 3'-phosphate through a carbonyl group attached
CC   to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethyl-
CC   pyrrolidine. The oligonucleotides form stable duplexes at physiological
CC   temperature and have selective cytotoxic activity against certain tumour
CC   cell lines, including some with multiple drug resistance.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGCG 19
               ||||||||
Db          8 CCCGTGCG 1


RESULT 60
AAZ80768/c
ID   AAZ80768 standard; DNA; 10 BP.
XX
AC   AAZ80768;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 58; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGC 12
              ||||||||
Db         10 CAGGGAGC 3


RESULT 61
AAZ82243/c
ID   AAZ82243 standard; DNA; 10 BP.
XX
AC   AAZ82243;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1477.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
```

```
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 98; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGG 8
              ||||||||
Db          9 GCTTCAGG 2


RESULT 62
AAZ82499
ID   AAZ82499 standard; DNA; 10 BP.
XX
AC   AAZ82499;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1733.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 105; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCC 14
              ||||||||
Db          2 GGGAGCCC 9


RESULT 63
AAZ83879
ID   AAZ83879 standard; DNA; 10 BP.
XX
AC   AAZ83879;
XX
DT   07-APR-2000  (first entry)
```

```
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3113.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 142; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGG 8
              ||||||||
Db          3 GCTTCAGG 10


RESULT 64
AAZ85236/c
ID   AAZ85236 standard; DNA; 10 BP.
XX
AC   AAZ85236;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4470.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 179; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGG 9
              ||||||||
Db         10 CTTCAGGG 3


RESULT 65
AAZ85403
ID   AAZ85403 standard; DNA; 10 BP.
```

```
XX
AC   AAZ85403;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4637.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 183; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAG 11
              ||||||||
Db          1 TCAGGGAG 8


RESULT 66
```

```
AAZ85929
ID   AAZ85929 standard; DNA; 10 BP.
XX
AC   AAZ85929;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5163.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US13647.
XX
PR   19-JUN-1998;   98US-0089853.
PR   19-JUN-1998;   98US-0089997.
PR   19-JUN-1998;   98US-0090039.
PR   19-JUN-1998;   98US-0090040.
PR   19-JUN-1998;   98US-0090041.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic
PT   and non-metastatic breast cancer cells, useful for diagnosis,
PT   prevention and treatment of cancer -
XX
PS   Claim 1; Page 196; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC   transcripts that are preferentially transcribed in the metastatic breast
CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the primary or non-metastatic
CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC   cells). These transcripts can be used for diagnosis, prognosis,
CC   monitoring and treatment of breast cancer, particularly where metastatic.
CC   Diagnosis is by standard immunoassays or hybridisation/amplification
CC   reactions. Compounds that modulate expression of the transcripts are
CC   potentially useful for treatment of (metastatic) breast cancer, while
CC   promoters from the transcripts are used to direct expression, in selected
CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC   sequences), particularly an antigen-encoding sequence for use in gene or
CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
CC   useful in vaccines; for diagnosing breast cancer and for raising
CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
CC   therapeutic agents. Host cells that produce the polypeptides can be used
CC   to expand and isolate populations of educated, antigen-specific immune
CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
CC   adoptive immunotherapy.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 4 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCC 14
              ||||||||
Db          1 GGGAGCCC 8
```

```
RESULT 67
AAH63615
ID   AAH63615 standard; cDNA; 10 BP.
XX
AC   AAH63615;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 455.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 49; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 GCCCGTGC 18
               ||||||||
Db           1 GCCCGTGC 8


RESULT 68
AAH64015/c
ID   AAH64015 standard; cDNA; 10 BP.
XX
AC   AAH64015;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 855.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US31922.
XX
PR   24-NOV-1999;   99US-0448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell
PT   type, such as cancer cell, comprises transcriptomes expressed in
PT   particular cell types -
XX
PS   Claim 13; Page 58; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences
CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
CC   in the invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of
CC   the transcriptomes described in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           4 TCAGGGAG 11
               ||||||||
Db           9 TCAGGGAG 2


RESULT 69
AAF97341/c
ID   AAF97341 standard; DNA; 10 BP.
XX
AC   AAF97341;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #2102.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(10,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US24503.
XX
PR   10-SEP-1999;   99US-0153357.
PR   26-JUL-2000; 2000US-0220947.
PR   16-AUG-2000; 2000US-0225724.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
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PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX
DR WPI; 2001-226749/23.
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis -
XX
PS Examples; Page 192; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPS shown in the specification.
XX
SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGGGAGC 12
||||||||
Db 9 CAGGGAGC 2

RESULT 70
AAF37906/c
ID AAF37906 standard; DNA; 10 BP.
XX
AC AAF37906;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4645.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 165; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCAGGGA 10
||||||||
Db 9 TTCAGGGA 2

RESULT 71
AAF42841/c
ID AAF42841 standard; DNA; 10 BP.
XX
AC AAF42841;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10980.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX

PS Example; Page 342; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGA 10
              ||||||||
Db          8 TTCAGGGA 1
```

RESULT 72
AAD44471/c
ID AAD44471 standard; DNA; 10 BP.
XX
AC AAD44471;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human F2RL1 gene polymorphisms detecting primer #9.
XX
KW Human; haplotype; coagulation factor II receptor like 1; F2RL1; asthma;
KW polymorphism; chronic pulmonary disease; inflammatory disorder;
KW gene therapy; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200255534-A2.
XX
PD 18-JUL-2002.
XX
PF 13-NOV-2001; 2001WO-US46475.
XX
PR 10-NOV-2000; 2000US-247516P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Sanchis A, Shah N;
XX
DR WPI; 2002-566728/60.
XX
PT New genetic variants having polymorphisms in the coagulation factor II
PT (thrombin) receptor like 1 (F2RL1) gene, useful for studying the
PT function of F2RL1 and treating disorders associated with abnormal
PT expression or function of F2RL1 -
XX
PS Claim 16; Page 14; 65pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising genes
CC and haplotypes of the coagulation factor II (thrombin) receptor like 1
CC (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in
CC studying the expression and biological function of F2RL1, and in
CC identifying drugs targetting F2RL1 protein for treating disorders
CC associated with abnormal expression or function of F2RL1, e.g. asthma,
CC chronic pulmonary disease, and inflammatory disorders. Polynucleotides
CC comprising a polymorphic gene variant or fragment may be used for
CC therapeutic purposes, where a patient could benefit from expression or
CC increased expression of a particular F2RL1 protein isoform, or an
CC expression vector encoding the isoform may be administered to the
CC patient. Haplotype information is useful in improving the efficiency and
CC output of several steps in drug discovery and development process,
CC including target validation, identifying lead compounds, and early phase
CC clinical trials. Information on polymorphisms may be applied in studying
CC biological functions of F2RL1 as well as in identifying drugs targetting
CC this protein for the treatment of disorders related to its abnormal
CC expression or function. The invention is useful in gene therapy. The
CC present sequence is human F2RL1 gene polymorphism detecting primer.
XX
SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGA 10
              ||||||||
Db          9 TTCAGGGA 2
```

RESULT 73
ABV84539/c
ID ABV84539 standard; cDNA; 10 BP.
XX
AC ABV84539;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human cDNA clone PLACE1000142 SAGE tag #349.
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; differential expression; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-0012328.
XX
PR 19-JAN-2001; 2001JP-0012328.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-631294/68.
XX
PT Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes -
XX
PS Claim 28; Page 20; 139pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced

```
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis
CC   C liver tissue or HCC, antibodies against these proteins, and inhibitors
CC   of the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84491-ABV84590 are SAGE tags representing the 100 least highly
CC   expressed genes out of those genes which are underexpressed in
CC   hepatocellular carcinoma compared with normal liver tissue.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGG 9
              ||||||||
Db          8 CTTCAGGG 1


RESULT 74
ABT05343
ID   ABT05343 standard; DNA; 10 BP.
XX
AC   ABT05343;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Human NAGA-alpha gene primer extension oligonucleotide 3.
XX
KW   Human; PCR; primer; ss; gene therapy; N-acetylgalactosaminidase alpha;
KW   chromosome 22q13.2-q13.31; lysosomal glycohydrolase; screening; SNP;
KW   NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
KW   genotyping.
XX
OS   Homo sapiens.
XX
PN   WO200194637-A1.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US18456.
XX
PR   07-JUN-2000; 2000US-210110P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kazemi A,  Koshy B,  Parks KE;
XX
DR   WPI; 2002-566449/60.
XX
PT   New genetic variants of isolated N-acetylgalactosaminidase (NAGA),
PT   Alpha gene, useful for therapeutic purposes, for studying the
PT   expression and function of the polynucleotide, and for expressing NAGA
PT   protein  -
XX
PS   Claim 18; Page 13; 91pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of the human
CC   N-acetylgalactosaminidase (NAGA) alpha protein. The invention
CC   specifically comprises novel polymorphic sites identified within the NAGA
CC   gene. The NAGA gene is located on chromosome 22q13.2-q13.31, and encodes
CC   a lysosomal glycohydrolase that cleaves alpha-N-acetylgalactosaminyl
CC   moieties in glycoconjugates. The NAGA DNA and protein sequences of the
CC   invention are useful for studying the expression and function of NAGA and
CC   for screening candidate drugs to treat diseases related to NAGA activity.
CC   The NAGA gene polymorphisms identified in the present invention are
CC   useful for haplotyping and genotyping the NAGA gene of an individual. The
CC   present DNA sequence represents an N-acetylgalactosaminidase gene primer
CC   extension oligonucleotide.
XX
SQ   Sequence 10 BP; 2 A; 4 C; 4 G; 0 U; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCC 14
              ||||||||
Db          2 GGGAGCCC 9


RESULT 75
ABK96539/c
ID   ABK96539 standard; DNA; 10 BP.
XX
AC   ABK96539;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human PLAU gene, primer extension primer 3' terminus #12.
XX
KW   Human; ss; primer; Plasminogen activator; urokinase; PLAU; cancer;
KW   cytostatic; serine protease; thrombolytic disorder; isogene; PCR;
KW   pulmonary embolism; chromosome 10q24-qter; haplotype; genotype;
KW   SNP; single nucleotide polymorphism; thrombolytic; gene therapy;
KW   primer extension.
XX
OS   Homo sapiens.
XX
PN   WO200240503-A2.
XX
PD   23-MAY-2002.
XX
PF   14-NOV-2001; 2001WO-US44001.
XX
PR   17-NOV-2000; 2000US-249703P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Bentivegna SC,  Koshy B;
XX
DR   WPI; 2002-519370/55.
XX
PT   Genetic variants of Plasminogen activator, Urokinase (PLAU) isogenes,
PT   useful for improving efficiency and reliability in drug development for
PT   treating thrombolytic disorders and cancer -
XX
PS   Claim 16; Page 14; 92pp; English.
XX
CC   The invention relates to a polynucleotide comprising a first nucleotide
CC   sequence (NS1) comprising a PLAU (plasminogen activator, urokinase,
CC   a serine protease) isogene selected from isogenes 1-9 and 11-20 given
CC   in the specification, where each isogene comprises the regions of the
CC   PLAU gene or cDNA and is further defined by the corresponding sequence of
CC   polymorphisms (defining single nucleotide polymorphisms, SNP). Also
CC   included are methods of haplotyping/genotyping (and predicting the
CC   haplotype/genotype of the  PLAU gene of an individual, identifying an
CC   association between a trait and at least one haplotype or haplotype pair
CC   of the PLAU gene, an isolated oligonucleotide for detecting a
CC   polymorphism in the PLAU gene, a recombinant non-human organism
CC   transformed or transfected with the gene or cDNA, fragments of the
CC   polynucleotides of at least 10 base pairs encompassing a polymorphic
CC   site, an isolated polymorphic variant PLAU protein or fragment, an
CC   isolated monoclonal antibody specific for PLAU, a computer system for
CC   storing and analysing polymorphism data for the PLAU gene and a genome
CC   anthology for the PLAU gene. PLAU is useful in screening for drugs
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CC   targeting PLAU that are useful for treating thrombolytic disorders and
CC   cancers. The methods are useful for improving the efficiency and
CC   reliability of the discovery and development of drugs for treating
CC   diseases associated with PLAU activity, in validating PLAU as a drug
CC   target and in the design of clinical trials for treating a specific
CC   condition of disease associated with PLAU activity. The antibody is
CC   useful in diagnostic, prognostic and therapeutic methods. PLAU
CC   polynucleotides are useful in studying the expression and function of
CC   PLAU, and in expressing PLAU protein for use in screening for candidate
CC   drugs to treat diseases related to PLAU activity. The gene for PLAU
CC   is located on chromosome 10q24-qter. The present sequence is the 3'
CC   terminus of an allele specific primer used to amplify PLAU
CC   polynucleotides with a specific polymorphism using the technique of
CC   primer extension.
XX
SQ   Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGGG 9
              ||||||||
Db         10 CTTCAGGG 3


RESULT 76
ABK85687/c
ID   ABK85687 standard; DNA; 10 BP.
XX
AC   ABK85687;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Human SCYB6 gene polymorphism detection oligonucleotide primer #8.
XX
KW   Human; small inducible cytokine subfamily B (Cys-X-Cys);
KW   Member 6 (granulocyte chemotactic protein 2); SCYB6; primer; ss;
KW   inflammatory disorder; cancer; antiinflammatory; cytostatic;
KW   gene therapy; SCYB6 isogene expression modulator; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200227030-A1.
XX
PD   04-APR-2002.
XX
PF   27-SEP-2001; 2001WO-US30413.
XX
PR   27-SEP-2000; 2000US-235809P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Bentivegna SC,  Choi JY,  Monroe G,  Russo DP;
XX
DR   WPI; 2002-405057/43.
XX
PT   New isolated polymorphic variant of small inducible cytokine subfamily
PT   B (Cys-X-Cys), Member 6 (granulocyte chemotactic protein 2) gene,
PT   useful for expressing protein isoform used in drug screening techniques
PT   -
XX
PS   Claim 16; Page 13; 71pp; English.
XX
CC   The present invention relates to a new polynucleotide having small
CC   inducible cytokine subfamily B (Cys-X-Cys), Member 6 (granulocyte
CC   chemotactic protein 2) (SCYB6) isogene. The invention is useful for
CC   studying expression and function of SCYB6 and expressing SCYB6 protein
CC   for use in screening for candidate drugs to treat diseases related to
CC   SCYB6 activity. The polymorphism and haplotype data is useful for
CC   validating whether SCYB6 is a suitable target for drugs to inflammatory
CC   disorders and cancer, screening for such drugs and reducing bias
CC   in clinical trials of such drugs. The invention is also useful for
CC   therapeutic purposes. The method of the invention is useful for
CC   identifying an association between susceptibility to a disease, staging
CC   of a disease, or response to a drug. The present nucleic acid sequence
CC   represents one of a collection of oligonucleotide primers (ABK85680-
CC   ABK85697) that were used in the invention to detect polymorphisms in
CC   the human SCYB6 gene.
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TTCAGGGA 10
              ||||||||
Db          8 TTCAGGGA 1


RESULT 77
ABA98387
ID   ABA98387 standard; DNA; 10 BP.
XX
AC   ABA98387;
XX
DT   30-JUL-2002  (first entry)
XX
DE   SCN2B gene polymorphisms oligonucleotide primer #13.
XX
KW   Human; sodium channel voltage gated type 2 beta polypeptide; SCN2B;
KW   ds; gene therapy; neuroprotective; demyelinating disease.
XX
OS   Homo sapiens.
XX
PN   WO200179547-A1.
XX
PD   25-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US10743.
XX
PR   13-APR-2000; 2000US-196597P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-075072/10.
XX
PT   New polynucleotide containing polymorphisms in the human sodium channel
PT   voltage gated type 2 beta polypeptide (SCN2B) gene, for developing
PT   drugs for treating demyelinating diseases  -
XX
PS   Claim 17; Page 13; 63pp; English.
XX
CC   This invention relates to an isolated polynucleotide which is a
CC   polymorphic variant of a reference sequence for sodium channel
CC   voltage gated type 2 beta polypeptide (SCN2B) gene. The methods have
CC   applicability in developing diagnostic tests and therapeutic treatments
CC   for demyelinating diseases. The protein is useful for studying the
CC   expression and function of SCN2B and expressing SCN2B protein for use
CC   in screening for candidate drugs to treat diseases related to SCN2B
CC   activity. The polymorphism and haplotype data are useful for validating
CC   whether SCN2B is a suitable target for drugs to treat demyelinating
CC   diseases, screening for such drugs and reducing bias in clinical
CC   trials. The haplotyping method is useful to validate SCN2B as a
CC   candidate target for treating a specific condition or disease predicted
CC   to be associated with SCN2B activity. A recombinant non-human organism
CC   transformed or transfected with the polypeptide is useful for studying
CC   expression of the SCN2B isogenes in vivo, for in vivo screening and
CC   testing of drugs against SCN2B protein and for testing the efficacy
CC   of therapeutic agents and compounds for demyelinating diseases in a
CC   biological system. This sequence is used during the detection of
CC   polymorphisms of the SCN2B gene.
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XX
SQ   Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGG 8
              ||||||||
Db          3 GCTTCAGG 10


RESULT 78
ABK70549
ID   ABK70549 standard; DNA; 10 BP.
XX
AC   ABK70549;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human G protein-coupled receptor 7 allele-specific primer #9.
XX
KW   Human; G protein-coupled receptor 7; GPR7; haplotyping; SNP;
KW   psychological disorder; neurological disorder; primer; PCR; ss;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200222644-A1.
XX
PD   21-MAR-2002.
XX
PF   17-SEP-2001; 2001WO-US29207.
XX
PR   15-SEP-2000; 2000US-232900P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Koshy B,  Sanchis A,  Tirrell C;
XX
DR   WPI; 2002-383121/41.
XX
PT   Novel genetic variants of G protein-coupled receptor 7 gene useful for
PT   therapeutic purposes and for expressing GPR7 protein useful in
PT   identifying drugs to treat psychological and neurological disorders  -
XX
PS   Claim 18; Page 13; 69pp; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising a
CC   nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for G-protein coupled receptor 7 (GPR7) gene or its fragment, or
CC   a polymorphic variant of a reference sequence for a GPR7 cDNA or its
CC   fragment. The encoded polypeptide (II) is useful for screening for drugs
CC   targeting the polypeptide. (I) is useful for identifying an association
CC   between a trait such as a clinical response to a drug targeting GPR7 and
CC   a haplotype or haplotype pair of GPR7 gene. Such methods have
CC   applicability in developing diagnostic tests and therapeutic treatments
CC   psychological and neurological disorders. (I) is useful for studying
CC   the expression and function of GPR7 and expressing GPR7 protein for use
CC   in screening for candidate drugs to treat diseases related to GPR7
CC   activity. The polymorphism and haplotype data are useful for validating
CC   whether GPR7 is a suitable target for drugs to treat psychological and
CC   neurological disorders, screening for such drugs and reducing bias in
CC   clinical trials of such drugs. (I) is useful for therapeutic purposes.
CC   Establishing the GPR7 haplotype or haplotype pair of an individual is
CC   useful for improving the efficiency and reliability of several steps in
CC   the discovery and development of drugs for treating diseases associated
CC   with GPR7 activity psychological and neurological disorders. The
CC   haplotyping method is useful to validate GPR7 as a candidate target for
CC   treating a specific condition or disease predicted to be associated with
CC   GPR7 activity. The method is also useful in screening for compounds
CC   targeting GPR7 to treat a specific condition or disease predicted to be
CC   associated with GPR7 activity, e.g. detecting which of the GPR7
CC   haplotypes or haplotype pairs present in individual members of a
CC   population with the specific disease of interest enables one to screen
CC   for compounds that display the highest desired agonist or antagonist
CC   activity for each of the most frequent GPR7 isoforms present in the
CC   disease population. A polymorphic variant of GPR7 is useful in studying
CC   the effect of the variation on the biological activity of GPR7, on the
CC   binding affinity of candidate drugs targeting GPR7 for the treatment of
CC   psychological and neurological disorders and in assays to measure the
CC   binding affinities of one or more candidate drugs targeting the GPR7
CC   protein. (I) is useful for studying expression of the GPR7 isogenes in
CC   vivo, for in vivo screening and testing of drugs against GPR7 protein
CC   and for testing the efficacy of therapeutic agents and compounds for
CC   psychological and neurological disorders in a biological system. Antibody
CC   to (II) is useful for diagnostic and prognostic formats and therapeutic
CC   methods, for immunoprecipitating (II) from solution, for detecting GPR7
CC   protein isoforms in biological samples, frozen tissue sections, cells
CC   which have been fixed or unfixed and prepared on slides, for use in
CC   immunocytochemical, immunohistochemical and immunofluorescence
CC   techniques. ABK70517-ABK70558 represent human GPR7 allele-specific
CC   probes and primers used in haplotyping of human GPR7 as described in the
CC   invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGG 8
              ||||||||
Db          1 GCTTCAGG 8


RESULT 79
ABL52211/c
ID   ABL52211 standard; DNA; 10 BP.
XX
AC   ABL52211;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Human PER1 preferred oligonucleotide primer SEQ ID NO:136.
XX
KW   Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW   polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW   single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200222650-A2.
XX
PD   21-MAR-2002.
XX
PF   13-SEP-2001; 2001WO-US28780.
XX
PR   13-SEP-2000; 2000US-232468P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Koshy B;
XX
DR   WPI; 2002-393941/42.
XX
PT   Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT   for therapeutic purposes, for studying the expression and function of
PT   the polynucleotide, and for expressing the homolog  -
XX
PS   Claim 19; Page 16; 162pp; English.
XX
CC   The present invention describes an isolated human period (Drosophila)
CC   homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC   polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC   or its fragment, or a polymorphic variant of a reference sequence
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CC   (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC   describes methods for genotyping and haplotyping the PER1 gene of an
CC   individual. (I) is useful in studying the expression and function of
CC   PER1, and in expressing PER1 protein for use in screening for candidate
CC   drugs to treat diseases related to PER1 activity. (I) is useful for
CC   therapeutic purposes. A recombinant non-human organism transformed or
CC   transfected with (I) can be used for studying expression of the PER1
CC   isogenes in vivo, for in vivo screening and testing of drugs targeted
CC   against PER1 protein, and for testing the efficacy of therapeutic agents
CC   and compounds for disorders associated with circadian rhythm regulation.
CC   The present sequence represents a preferred oligonucleotide primer
CC   for human PER1, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCC 14
              ||||||||
Db         10 GGGAGCCC 3


RESULT 80
ABL52257/c
ID   ABL52257 standard; DNA; 10 BP.
XX
AC   ABL52257;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human PHKG2 preferred oligonucleotide primer SEQ ID NO:44.
XX
KW   Human; phosphorylase kinase gamma 2 (testis); PHKG2; enzyme; SNP;
KW   phosphorylase kinase gamma 2; single nucleotide polymorphism;
KW   polymorphic; hepatotropic; gene therapy; glycogen storage disease;
KW   liver cirrhosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200194365-A2.
XX
PD   13-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US18814.
XX
PR   09-JUN-2000; 2000US-210568P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Koshy B,  Sanchis A,  Sausker EA;
XX
DR   WPI; 2002-401587/43.
XX
PT   New variants of phosphorylase kinase gamma 2 isogenes, useful for
PT   improving efficiency and reliability in the development of drugs for
PT   treating diseases e.g. liver cirrhosis  -
XX
PS   Claim 18; Page 14; 76pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) comprising
CC   a nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for human phosphorylase kinase gamma2 (testis) (PHKG2) gene or
CC   its fragment, or a polymorphic variant of a reference sequence for a
CC   PHKG2 cDNA or its fragment. Also described is an isolated polypeptide
CC   (II) comprising an amino acid sequence which is a polymorphic variant of
CC   a reference sequence for PHKG2 protein or its fragment, where the
CC   reference sequence comprises a sequence (see ABB09290) of 406 amino
CC   acids, and the polymorphic variant comprises one or more variant amino
CC   acids selected from glutamic acid at a position corresponding to amino
CC   acid position 153 and tryptophan at position corresponding to amino acid
CC   position 329. (I) has hepatotropic activity and can be used in gene
CC   therapy. (II) is useful in screening for drugs targeting (II), by
CC   contacting a PHKG2 polymorphic variant with a candidate agent and
CC   assaying for binding activity. The identified candidate agents targeting
CC   PHKG2, are useful for treating liver cirrhosis and glycogen storage
CC   diseases. The present sequence represents a preferred oligonucleotide
CC   primer for the PHKG2 gene, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGG 8
              ||||||||
Db         10 GCTTCAGG 3


RESULT 81
ABK23463/c
ID   ABK23463 standard; DNA; 10 BP.
XX
AC   ABK23463;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #52 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL00361.
XX
PR   11-MAY-2000; 2000EP-0201698.
PR   29-JUN-2000; 2000EP-0202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer  -
XX
PS   Disclosure; Page 50; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising
CC   myc-dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified
CC   by SAGE (serial analysis of gene expression). The library is useful to
CC   find new diagnoses and treatments for cancer. The invention is also
CC   useful to enhance production of recombinant proteins in a production
CC   system with high expression of endogenous or transfected myc oncogenes.
CC   ABK23412-ABK23828 represent transcript tag DNA sequences that are
CC   activated or repressed by N-myc in human neuroblastoma.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          5 CAGGGAGC 12
              ||||||||
Db         10 CAGGGAGC 3
```

RESULT 82
AAD26187
ID AAD26187 standard; DNA; 10 BP.
XX
AC AAD26187;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human endothelin 2 (EDN2) gene polymorphism detecting primer #26.
XX
KW Human; endothelin 2; EDN2; polymorphic site; PS; therapy; hypertension;
KW drug screening; cardiovascular disorder; renal insufficiency; ASO;
KW allele specific oligonucleotide; cerebroprotective; polymorphism;
KW hypotensive; cerebrovascular condition; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190118-A2.
XX
PD 29-NOV-2001.
XX
PF 21-MAY-2001; 2001WO-US16433.
XX
PR 19-MAY-2000; 2000US-205761P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Koshy B, Tanguay DA;
XX
DR WPI; 2002-083075/11.
XX
PT New human endothelin 2 (EDN2) polymorphic variants and encoding genes,
PT useful in expressing EDN2 protein for screening candidate drugs to
PT treat diseases related to EDN2 activity -
XX
PS Claim 18; Page 15; 91pp; English.
XX
CC The invention relates to genetic variants of human endothelin 2 (EDN2)
CC gene. EDN2 gene contains 17 polymorphic sites PS1-PS17. The polymorphic
CC variants are useful in studying the expression and function of EDN2,
CC in expressing EDN2 protein for use in screening for candidate drugs to
CC treat diseases related to EDN2 activity, in studying the effect of the
CC variation on the biological activity of EDN2, and the binding affinity
CC of candidate drugs targetting EDN2 for the treatment of hypertension,
CC cardiovascular disorders, renal insufficiency and cerebrovascular
CC conditions. The haplotyping methods are useful in validating EDN2 as
CC a candidate target for treating a specific condition or disease
CC predicted to be associated with EDN2 activity, or in the design of
CC clinical trials of candidate drugs for treating a specific condition
CC or disease associated with EDN2 activity. Allele specific
CC oligonucleotides (ASO) are used as probes and primers, and for
CC detecting polymorphism in EDN2 gene. The present sequence is a
CC primer used to detect polymorphism in human EDN2 gene.
XX
SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 U; 0 other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAGC 12
              ||||||||
Db          3 CAGGGAGC 10
```

RESULT 83
AAS19975
ID AAS19975 standard; DNA; 10 BP.
XX
AC AAS19975;
XX
DT 26-MAR-2002 (first entry)
XX
DE Primer-extension oligonucleotide #27 to detect human DNAL4 polymorphisms.
XX
KW Human; single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;
KW dynein axonemal light polypeptide chain 4; haplotyping; genotyping;
KW neuroprotective; neurological disorder; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200179235-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US12304.
XX
PR 17-APR-2000; 2000US-197460P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075065/10.
XX
PT Genotyping human dynein, axonemal light polypeptide chain 4 gene of
PT individual, useful for determining haplotype of individual, comprises
PT determining identity of nucleotide pair at specific polymorphic sites
PT for two copies of gene -
XX
PS Claim 18; Page 14; 79pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4)
CC gene located on chromosome 22q13.1, and methods for haplotyping and/or
CC genotyping the DNAL4 gene. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the DNAL4 gene
CC polymorphisms. The polynucleotides and screened compounds are useful
CC for the treatment of diseases associated with DNAL4 activity, such as
CC neurological disorders. AAS19949-AAS19976 represent primer-extension
CC oligonucleotides for detecting human DNAL4 gene polymorphisms.
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCCC 14
              ||||||||
Db          2 GGGAGCCC 9
```

RESULT 84
ABL39540
ID ABL39540 standard; DNA; 10 BP.
XX
AC ABL39540;
XX
DT 22-APR-2002 (first entry)
XX
DE Human ETFB primer-extension oligonucleotide 46.
XX
KW Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW primer-extension oligonucleotide; single nucleotide polymorphism;
KW SNP.

XX
OS Homo sapiens.
XX
PN WO200202580-A2.
XX
PD 10-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US21306.
XX
PR 05-JUL-2000; 2000US-215984P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
XX
DR WPI; 2002-154722/20.
XX
PT Novel isolated human electron-transfer-flavoprotein, beta
PT polynucleotide, useful for therapeutic purposes, for studying the
PT expression and function of the polynucleotide, and for expressing the
PT flavoprotein -
XX
PS Claim 19; Page 15; 143pp; English.
XX
CC The invention comprises DNA, cDNA and protein sequences of the human
CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC chromosome 19q13.3-13.4). The invention specifically relates to the
CC identification of 27 novel polymorphic sites within the ETFB gene.
CC Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC for nine primary flavoprotein dehydrogenases and is located in the
CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC GAII. The novel ETFB polymorphisms identified in the invention are useful
CC for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC protein and nucleic acids of the invention are useful for studying the
CC expression and function of ETFB in vivo. The ETFB protein and nucleic
CC acids are also useful for testing the efficacy of therapeutic agents and
CC compounds for glutaric acidaemia type II. The nucleic acids of the
CC invention are useful in the production of a transgenic animal expressing
CC the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent
CC claimed ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC represent claimed ETFB primer-extension oligonucleotides.
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGG 8
              ||||||||
Db          3 GCTTCAGG 10
```

RESULT 85
ABT14248
ID ABT14248 standard; DNA; 10 BP.
XX
AC ABT14248;
XX
DT 20-FEB-2003 (first entry)
XX
DE Nucleic acid PCR amplification method-related RAPD PCR primer #18.
XX
KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS Unidentified.
XX
PN WO200281743-A2.
XX
PD 17-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-GB01489.
XX
PR 02-APR-2001; 2001GB-0008182.
XX
PA (HAMI/) HAMILL B.
XX
PI Hamill B;
XX
DR WPI; 2003-075484/07.
XX
PT Amplification of nucleotide sequences from polynucleotides by chain
PT extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT solution, 2 attached to supports and both share complementary sequences
PT -
XX
PS Disclosure; Fig 17; 60pp; English.
XX
CC The invention comprises a method for the PCR amplification of nucleic
CC acids. The method involves a set of primers, where two of the primers are
CC in solution and at least two other primers are attached to a solid
CC support. The method of the invention can be used for the analysis of a
CC nucleic acid or a mixture of nucleic acids, including: single-stranded
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC PCR primer of the invention.
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 other;

```
  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGGGAG 11
              ||||||||
Db          1 TCAGGGAG 8
```

RESULT 86
AAX54701
ID AAX54701 standard; DNA; 9 BP.
XX
AC AAX54701;
XX
DT 05-JUL-1999 (first entry)
XX
DE Muscarinic acetylcholine receptor H31 antisense oligonucleotide.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US19419.
XX
PR 09-JUN-1998; 98US-0093972.
PR 17-SEP-1997; 97US-0059160.
XX

PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
PS Disclosure; Page 54; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAX55272-74. These multiple target
CC oligonucleotides (specifically AAX55180-271) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;

```
  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CCCGTGCGG 20
              |||| ||||
Db          1 CCCGGGCGG 9
```

RESULT 87
AAF20270
ID AAF20270 standard; DNA; 9 BP.
XX
AC AAF20270;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human muscarinic acetylcholine receptor HM3 DNA fragment #1837.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.

XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 220; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;

```
  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 CCCGTGCGG 20
              |||| ||||
Db          1 CCCGGGCGG 9
```

RESULT 88
AAA34148
ID AAA34148 standard; DNA; 9 BP.
XX
AC AAA34148;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1837.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 494; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 9 BP; 0 A; 4 C; 5 G; 0 U; 0 other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCCGTGCGG 20
|||| ||||
Db 1 CCCGGGCGG 9

RESULT 89
ABQ71834
ID ABQ71834 standard; DNA; 9 BP.
XX
AC ABQ71834;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2132.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 56; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 1 A; 2 C; 5 G; 1 T; 0 other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTCAGGG 9
||| |||||
Db 1 GCTGCAGGG 9

RESULT 90
ABQ71835
ID ABQ71835 standard; DNA; 9 BP.
XX
AC ABQ71835;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2133.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 56; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 1 A; 2 C; 5 G; 1 T; 0 other;

```
  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 91
ABQ71836
ID ABQ71836 standard; DNA; 9 BP.
XX
AC ABQ71836;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2134.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 56; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 1 A; 2 C; 5 G; 1 T; 0 other;

```
  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 92
ABQ71837
ID ABQ71837 standard; DNA; 9 BP.
XX
AC ABQ71837;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2135.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX

PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 56; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 1 A; 2 C; 5 G; 1 T; 0 other;

```
  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTTCAGGG 9
              ||| |||||
Db          1 GCTGCAGGG 9
```

RESULT 93
AAT09588
ID AAT09588 standard; DNA; 8 BP.
XX
AC AAT09588;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1996 (first entry)
XX
DE 3'-primer used for characterisation of human biological samples.
XX
KW 3'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PT used for genome mapping and disease diagnosis
XX
PS Disclosure; Page 19; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer
CC kit with 1361 possible primer pairs. The kit is used in a new method
CC for the characterisation of nucleic acid sequences obtd. from human
CC biological samples, which comprises PCR amplification and indexing of
CC the prods. w.r.t the primer pair that hybridised to its delineating
CC subsequences. The method may be used in the identification, cloning
CC and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 BP; 1 A; 3 C; 2 G; 2 T; 0 other;

```
  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAG 7
              |||||||
Db          1 GCTTCAG 7
```

RESULT 94
AAT09371/c
ID AAT09371 standard; DNA; 8 BP.
XX
AC AAT09371;
XX
DT 25-MAR-2003 (updated)
DT 21-JUN-1996 (first entry)
XX
DE 5'-primer used for characterisation of human biological samples.
XX
KW 5'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PT used for genome mapping and disease diagnosis
XX
PS Claim 5; Page 44; 72pp; English.

```
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 3 A; 2 C; 2 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGG 8
              |||||||
Db          8 CTTCAGG 2


RESULT 95
AAT09466/c
ID   AAT09466 standard; DNA; 8 BP.
XX
AC   AAT09466;
XX
DT   25-MAR-2003  (updated)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 2 A; 2 C; 3 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAG 7
              |||||||
Db          8 GCTTCAG 2


RESULT 96
AAT09425/c
ID   AAT09425 standard; DNA; 8 BP.
XX
AC   AAT09425;
XX
DT   25-MAR-2003  (updated)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US06032.
XX
PR   16-MAY-1994;   94US-0242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers
PT   used for genome mapping and disease diagnosis
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer
CC   kit with 1361 possible primer pairs. The kit is used in a new method
CC   for the characterisation of nucleic acid sequences obtd. from human
CC   biological samples, which comprises PCR amplification and indexing of
CC   the prods. w.r.t the primer pair that hybridised to its delineating
CC   subsequences. The method may be used in the identification, cloning
CC   and analysis of genes, e.g. in genome mapping, and disease
CC   diagnosis.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 2 A; 2 C; 3 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGG 8
              |||||||
Db          7 CTTCAGG 1


RESULT 97
AAT09562
ID   AAT09562 standard; DNA; 8 BP.
```

XX
AC AAT09562;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1996 (first entry)
XX
DE 3'-primer used for characterisation of human biological samples.
XX
KW 3'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PT used for genome mapping and disease diagnosis
XX
PS Disclosure; Page 19; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer
CC kit with 1361 possible primer pairs. The kit is used in a new method
CC for the characterisation of nucleic acid sequences obtd. from human
CC biological samples, which comprises PCR amplification and indexing of
CC the prods. w.r.t the primer pair that hybridised to its delineating
CC subsequences. The method may be used in the identification, cloning
CC and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 BP; 1 A; 2 C; 2 G; 3 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCAGG 8
|||||||
Db 1 CTTCAGG 7

RESULT 98
AAT09544
ID AAT09544 standard; DNA; 8 BP.
XX
AC AAT09544;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1996 (first entry)
XX
DE 3'-primer used for characterisation of human biological samples.
XX
KW 3'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers
PT used for genome mapping and disease diagnosis
XX
PS Disclosure; Page 19; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer
CC kit with 1361 possible primer pairs. The kit is used in a new method
CC for the characterisation of nucleic acid sequences obtd. from human
CC biological samples, which comprises PCR amplification and indexing of
CC the prods. w.r.t the primer pair that hybridised to its delineating
CC subsequences. The method may be used in the identification, cloning
CC and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 BP; 1 A; 3 C; 2 G; 2 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCAGG 8
|||||||
Db 2 CTTCAGG 8

RESULT 99
AAX78349
ID AAX78349 standard; DNA; 8 BP.
XX
AC AAX78349;
XX
DT 25-AUG-1999 (first entry)
XX
DE Electrochemical detection octamer 1.
XX
KW Probe; oligomer; photoinducible redox-active unit; electron donor;
KW electron acceptor; conductive surface; detection; hybridisation; ss.
XX
OS Synthetic.
XX
PN DE19901761-A1.
XX
PD 01-JUL-1999.
XX
PF 18-JAN-1999; 99DE-1001761.
XX
PR 18-JAN-1999; 99DE-1001761.
XX
PA (HART/) HARTWICH G.
XX
PI Hartwich G;
XX
DR WPI; 1999-372624/32.
XX

```
PT   Oligonucleotides tagged with photoinducible redox-active unit - for
PT   binding to conductive surfaces for electrochemical detection of
PT   hybridisation
XX
PS   Disclosure; Fig 1; 28pp; German.
XX
CC   This invention describes a novel nucleic acid oligomer with a
CC   photoinducible redox-active unit which comprises one or more electron
CC   donors and one or more electron acceptors covalently attached. Probes
CC   comprising single-stranded DNA, RNA or PNA (peptide nucleic acid)
CC   oligomers linked at one end to a conductive surface and at the other end
CC   to a photoinducible redox-active unit can be used to detect hybridisation
CC   of a target oligonucleotides. This is possible because hybridisation
CC   increases the electrical communication between the conductive surface and
CC   the photoinducible redox-active unit. The probes may also be used for
CC   sequencing and detection of mismatched base pairs.
XX
SQ   Sequence 8 BP; 3 A; 1 C; 3 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGGGA 10
              |||||||
Db          1 TCAGGGA 7


RESULT 100
AAX29509/c
ID   AAX29509 standard; DNA; 8 BP.
XX
AC   AAX29509;
XX
DT   03-JUN-1999  (first entry)
XX
DE   Primer for human nuclear receptor genes.
XX
KW   Nucleic acid amplification; nuclear receptor; G-protein coupled receptor;
KW   apoptosis; DNA repair; DNA replication; plant biology; agriculture;
KW   human; veterinary medicine; reproduction; microbiology; hybridisation;
KW   environmental science; DNA fingerprinting; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9911823-A2.
XX
PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US18392.
XX
PR   05-SEP-1997;   97US-0925816.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   McClelland M,  Pesole G;
XX
DR   WPI; 1999-205200/17.
XX
PT   Subset of primers able to amplify group of related sequences
XX
PS   Claim 17; Page 74; 92pp; English.
XX
CC   The invention provides primers (AAX29501-X29679) for identifying
CC   sequences encoding structurally or functionally related proteins such as
CC   nuclear or G-protein coupled receptors, apoptosis-related or DNA
CC   repair/replication proteins. The identified sequences are broadly useful
CC   in plant biology, agriculture, human or veterinary medicine,
CC   reproduction, microbiology or environmental science, e.g. to study
CC   expression of nuclear receptors at different stages of tissue development
CC   or after treatment with particular drugs. It is also used for DNA
CC   fingerprinting (to generate products useful for differential
CC   hybridisation), or, where a 3'-anchor primer is used, to isolate the
CC   3'-ends of mRNA sequences. Sequences AAX29501-X29525 represent claimed
CC   primers specific for human nuclear receptor genes.
XX
SQ   Sequence 8 BP; 0 A; 4 C; 2 G; 2 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGGGAG 11
              |||||||
Db          7 CAGGGAG 1


RESULT 101
AAA80773
ID   AAA80773 standard; DNA; 8 BP.
XX
AC   AAA80773;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 86.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-0859954.
XX
PR   15-APR-1996;   96US-0632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction
PT   and other primer processes comprises primer walking of octamer
PT   oligonucleotides  -
XX
PS   Example 8; Column 67-68; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and
CC   corresponding complementary sequences, where the library primer is
CC   complementary to a known sequence adjacent to the unknown sequence or
CC   is complementary to a sequence in a known extension product. The method
CC   is useful for DNA nucleotide sequencing, in PCR, and in other processes
CC   which make use of primers.  The octamers are used to identify coding
CC   sequences. Primer walking using the octamer libraries is advantageous
CC   over other sequencing methods because it does not require multiple
CC   cloning steps nor subsequent template preparations, and it is a
CC   directed and methodical approach. AAA80688-A81253 represent the octamer
CC   primers used in the primer walking method of the invention.
XX
SQ   Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTTCAG 7
              |||||||
Db          1 GCTTCAG 7
```

```
RESULT 102
AAA81033/c
ID   AAA81033 standard; DNA; 8 BP.
XX
AC   AAA81033;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 346.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-0859954.
XX
PR   15-APR-1996;   96US-0632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction
PT   and other primer processes comprises primer walking of octamer
PT   oligonucleotides  -
XX
PS   Example 8; Column 199-200; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and
CC   corresponding complementary sequences, where the library primer is
CC   complementary to a known sequence adjacent to the unknown sequence or
CC   is complementary to a sequence in a known extension product. The method
CC   is useful for DNA nucleotide sequencing, in PCR, and in other processes
CC   which make use of primers.  The octamers are used to identify coding
CC   sequences. Primer walking using the octamer libraries is advantageous
CC   over other sequencing methods because it does not require multiple
CC   cloning steps nor subsequent template preparations, and it is a
CC   directed and methodical approach. AAA80688-A81253 represent the octamer
CC   primers used in the primer walking method of the invention.
XX
SQ   Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGG 8
              |||||||
Db          7 CTTCAGG 1


RESULT 103
AAA81034/c
ID   AAA81034 standard; DNA; 8 BP.
XX
AC   AAA81034;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 347.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-0859954.
XX
PR   15-APR-1996;   96US-0632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction
PT   and other primer processes comprises primer walking of octamer
PT   oligonucleotides  -
XX
PS   Example 8; Column 199-200; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and
CC   corresponding complementary sequences, where the library primer is
CC   complementary to a known sequence adjacent to the unknown sequence or
CC   is complementary to a sequence in a known extension product. The method
CC   is useful for DNA nucleotide sequencing, in PCR, and in other processes
CC   which make use of primers.  The octamers are used to identify coding
CC   sequences. Primer walking using the octamer libraries is advantageous
CC   over other sequencing methods because it does not require multiple
CC   cloning steps nor subsequent template preparations, and it is a
CC   directed and methodical approach. AAA80688-A81253 represent the octamer
CC   primers used in the primer walking method of the invention.
XX
SQ   Sequence 8 BP; 3 A; 2 C; 2 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTTCAGG 8
              |||||||
Db          7 CTTCAGG 1


RESULT 104
AAQ37100
ID   AAQ37100 standard; DNA; 9 BP.
XX
AC   AAQ37100;
XX
DT   25-MAR-2003  (updated)
DT   23-JUN-1993  (first entry)
XX
DE   Phoma lingam pathotype differentiation primer.
XX
KW   Aggressive; non-aggressive; early stage; rape; cruciferous;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   DE4127862-A1.
XX
PD   25-FEB-1993.
XX
PF   21-AUG-1991;   91DE-4127862.
XX
PR   21-AUG-1991;   91DE-4127862.
XX
```

PA (GENB-) INST GENBIOLOGISCHE FORSCHUNG.
XX
PI Schaefer C, Woestemeyer J;
XX
DR WPI; 1993-067990/09.
XX
PT Aggressive and non-aggressive pathotype distinction of Phoma
PT lingam - using random primers of 8-11 nucleotide(s) giving differing
PT pattern after gel-electrophoresis, useful in plant protection
XX
PS Claim 3; Page 5; 8pp; German.
XX
CC The sequence is that of a PCR primer used as part of a method for
CC differentiation between aggressive and non-aggressive pathotypes of
CC Phoma lingam (Leptosphaeria maculans) at an early stage and in a
CC quick and easy manner. The different pathotypes can thus be
CC distinguished in cruciferous plants, esp. in rape, without using
CC radioactivity.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 BP; 2 A; 4 C; 3 G; 0 U; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGAGCCC 14
|||||||
Db 1 GGAGCCC 7

RESULT 105
AAT27993/c
ID AAT27993 standard; DNA; 9 BP.
XX
AC AAT27993;
XX
DT 16-DEC-1996 (first entry)
XX
DE Monoclonal antibody B3 light chain coding sequence fragment.
XX
KW Antibody; fusion protein; single chain; inhibition; tumour;
KW diagnosis; detection; imaging; immunotoxin; targetting; assay;
KW immunoassay; Lewis(Y) carbohydrate antigen; ss.
XX
OS Mus musculus.
XX
PN WO9613594-A1.
XX
PD 09-MAY-1996.
XX
PF 26-OCT-1995; 95WO-US13811.
XX
PR 28-OCT-1994; 94US-0331398.
PR 28-OCT-1994; 94US-0331396.
PR 28-OCT-1994; 94US-0331397.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;
PI Padlan EA, Pai L, Pastan I, Willingham M;
XX
DR WPI; 1996-251462/25.
XX
PT Single chain fusion proteins and antibodies - useful to diagnose and
PT treat cancer, specifically bind Lewis(Y) related carbohydrate
PT antigen
XX
PS Disclosure; Page 7; 116pp; English.
XX
CC A novel recombinant DNA molecule which encodes a single chain fusion
CC protein or antibody comprising the Fv region of both the light and
CC heavy chains of an antibody (Ab) fused together, and an effector
CC molecule, where the fusion protein or Ab has the binding specificity
CC of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production
CC of such fusion proteins or antibodies. The fusion proteins can be
CC used in compositions as an immunotoxin to inhibit tumour cell growth.
CC The single chain antibody can be used to detect the presence or
CC absence of cells bearing a Lewis(Y) carbohydrate antigen in a
CC patient. The antibodies are also useful as multiple targetting
CC moieties, providing at least 2 kinds of biological activity. They
CC can also be used in diagnostic assays and for the imaging of tumours
CC when attached to a radiolabel and for the pathological diagnosis of
CC tumours. Humanised antibodies are less immunogenic than the mouse
CC MAbs B1, B3 and B5, making them more suitable for long term
CC treatment.
XX
SQ Sequence 9 BP; 0 A; 5 C; 1 G; 3 T; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGGGAG 11
|||||||
Db 9 CAGGGAG 3

RESULT 106
ABQ71823
ID ABQ71823 standard; DNA; 9 BP.
XX
AC ABQ71823;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2121.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 56; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the

CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 3 A; 1 C; 5 G; 0 U; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 CAGGGAG 11
              |||||||
Db          1 CAGGGAG 7
```

RESULT 107
ABQ71824
ID ABQ71824 standard; DNA; 9 BP.
XX
AC ABQ71824;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2122.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 56; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 3 A; 1 C; 5 G; 0 U; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 CAGGGAG 11
              |||||||
Db          1 CAGGGAG 7
```

RESULT 108
ABQ71874
ID ABQ71874 standard; DNA; 9 BP.
XX
AC ABQ71874;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2172.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 57; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity

CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 1 A; 2 C; 6 G; 0 U; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GGGAGCC 13
|||||||
Db 3 GGGAGCC 9

RESULT 109
ABQ71875
ID ABQ71875 standard; DNA; 9 BP.
XX
AC ABQ71875;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2173.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 57; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 1 A; 2 C; 6 G; 0 U; 0 other;

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GGGAGCC 13
|||||||
Db 3 GGGAGCC 9

RESULT 110
ABQ71888
ID ABQ71888 standard; DNA; 9 BP.
XX
AC ABQ71888;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2186.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US43438.
XX
PR 20-NOV-2000; 2000US-0716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering,
PT comprises first, second and third zinc fingers, ordered from N- to
PT C-terminus -
XX
PS Example 1; Page 57; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to
CC a target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC it binds to the S1 target subsite, selecting the F2 zinc finger such
CC that it binds to the S2 target subsite, and selecting the F3 zinc
CC finger such that it binds to the S3 target subsite, thus designing (I)
CC that binds to a target site. (I) is useful for recognition of triplet
CC target subsites having the nucleotide G in the 5'-most position of the
CC subsite. (I) is useful in studying gene function, and for human
CC therapeutics and plant engineering. (I), (II) or (III) is useful in
CC therapeutic methods to modulate the expression of a target region within
CC a subject, in diagnostic methods for sequence specific detection of
CC target nucleic acid in a sample, and in assays to determined the
CC phenotype and function of gene expression. (I) has improved affinity
CC and specificity for their target sequences, as well as enhanced
CC biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC represent DNA target sequences and zinc finger peptides which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 9 BP; 2 A; 2 C; 5 G; 0 U; 0 other;

```
  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 111
ABQ71889
ID   ABQ71889 standard; DNA; 9 BP.
XX
AC   ABQ71889;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2187.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US43438.
XX
PR   20-NOV-2000; 2000US-0716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering,
PT   comprises first, second and third zinc fingers, ordered from N- to
PT   C-terminus  -
XX
PS   Example 1; Page 57; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
CC   and specificity for their target sequences, as well as enhanced
CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC   represent DNA target sequences and zinc finger peptides which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 9 BP; 2 A; 2 C; 5 G; 0 U; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 112
ABQ71908
ID   ABQ71908 standard; DNA; 9 BP.
XX
AC   ABQ71908;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2206.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US43438.
XX
PR   20-NOV-2000; 2000US-0716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering,
PT   comprises first, second and third zinc fingers, ordered from N- to
PT   C-terminus  -
XX
PS   Example 1; Page 57; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
CC   and specificity for their target sequences, as well as enhanced
CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC   represent DNA target sequences and zinc finger peptides which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 9 BP; 1 A; 2 C; 5 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
```

```
Db          3 GGGAGCC 9


RESULT 113
ABQ71946
ID   ABQ71946 standard; DNA; 9 BP.
XX
AC   ABQ71946;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2244.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US43438.
XX
PR   20-NOV-2000; 2000US-0716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering,
PT   comprises first, second and third zinc fingers, ordered from N- to
PT   C-terminus  -
XX
PS   Example 1; Page 58; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to
CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
CC   that it binds to the S2 target subsite, and selecting the F3 zinc
CC   finger such that it binds to the S3 target subsite, thus designing (I)
CC   that binds to a target site. (I) is useful for recognition of triplet
CC   target subsites having the nucleotide G in the 5'-most position of the
CC   subsite. (I) is useful in studying gene function, and for human
CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
CC   therapeutic methods to modulate the expression of a target region within
CC   a subject, in diagnostic methods for sequence specific detection of
CC   target nucleic acid in a sample, and in assays to determined the
CC   phenotype and function of gene expression. (I) has improved affinity
CC   and specificity for their target sequences, as well as enhanced
CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
CC   represent DNA target sequences and zinc finger peptides which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 9 BP; 1 A; 2 C; 5 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGGAGCC 13
              |||||||
Db          3 GGGAGCC 9


RESULT 114
AAD53774/c
ID   AAD53774 standard; DNA; 9 BP.
XX
AC   AAD53774;
XX
DT   28-MAY-2003  (first entry)
XX
DE   TACI related oligonucleotide.
XX
KW   Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW   TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW   anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW   glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW   dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW   autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW   diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; ss.
XX
OS   Unidentified.
XX
PN   WO200294852-A2.
XX
PD   28-NOV-2002.
XX
PF   20-MAY-2002; 2002WO-US15910.
XX
PR   24-MAY-2001; 2001US-293343P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Rixon MW,  Gross JA;
XX
DR   WPI; 2003-148455/14.
XX
PT   Transmembrane activator and calcium modulator and cyclophilin
PT   ligand-interactor (TACI)-immunoglobulin fusion protein, for treating
PT   cancer or diabetes, comprises a TACI receptor group and an
PT   immunoglobulin group -
XX
PS   Disclosure; Column 7; 71pp; English.
XX
CC   The invention relates to fusion proteins comprising transmembrane
CC   activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC   receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
CC   ZTNF4; and an immunoglobulin group comprising a constant region of an
CC   immunoglobulin. The invention is used to manufacture a medicament for
CC   inhibiting the proliferation of tumour cells in a mammalian subject.
CC   The composition comprising the fusion protein may also be used in
CC   treating autoimmune diseases (e.g. systemic lupus erythematosus,
CC   multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma),
CC   renal diseases (e.g. glomerulonephritis), bronchitis, inflammation,
CC   graft rejection, anaemia and septic shock. The fusion proteins are
CC   also used in gene therapy. The present sequence is TACI related oligo
CC   used in the invention.
XX
SQ   Sequence 9 BP; 2 A; 2 C; 4 G; 1 T; 0 other;

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CCCGTGC 18
              |||||||
Db          9 CCCGTGC 3


Search completed: November 17, 2003, 09:12:52
Job time : 0.001 secs
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